```
probable phosphoglucomutase - syphilis spirochete

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: C71327

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwn rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MulD:98332770; PMID:9665876

A;Accession: C71327

A;Residues: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-632 <CCL>
A;Cross-references: UNIPROT:083428; GB:AE001219; GB:AE000520; NID:93322693; PIDN:AACG54

A;Experimental source: strain Nichols
                                                                                                                                                                                                                                   A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q8UHS4; GB:AE008688; PIDN:AAL41622.1; PID:g17738961; GSPDB:
A;Experimental source: strain C58 (Dupont)
A;Experimental source: strain C58 (Dupont)
A;Gene: Atu0605
A;Map position: circular chromosome
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: 697432
C;Accession: 697432
R;Goodner, B.: Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldmar
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to
A;Reference mumber: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transcription regulator (PA1138) [imported] - Agrobacterium tumefaciens (strai
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; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                             ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Reference number: AB2577; MUID:21608550; PMID:11743193
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37.1%; Score 46; DB 2; Length 290;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 1; Indels
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Pred. No. 24;
3; Mismatches
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A,Gene: AGR C_1075
A,Map position: circular chromosome
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66.7%;
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279 SDLYAGRKSRPA 290
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Best Local Similarity 66.7
Matches 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-290 <KUR>
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E7063
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Brosch, R.; Peltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. R;Jandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Julston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Retus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: UNA
A;Reterences: UNIPROT: P95206; GB: 284725; GB: AL123456; NID: G3261703; PIDN: CAB06589.
A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetical protein Rv0398c
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                                                                                                                                                                                                                                                                                                 5 [imported] - garden snapdragon (fragment)
                                                                                                                                                                                                                                                                                 Squamosa promoter binding protein-homolog 5 [imported] - garden snapdragon (fragme CjSpecies: Antirrhinum majus (garden snapdragon)
CjSpecies: Antirrhinum majus (garden snapdragon)
CjSpecies: O-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
CjAccession: T52297
R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P. R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P. A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Reference number: Z5236; MUID:99453765; PMID:10524240
A;Reference number: Z5236; MUID:99453765; PMID:10524240
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-323 <CAR>
A;Residues: 1-323 <CAR>
A;Residues: 1-323 <CAR>
A;Residues: 1-324 <CAR>
A;Residues: 1-324 <CAR>
A;Residues: 1-325 <CAR>
A;Residues: 1-325 <CAR>
A;Gross-references: UNIPROT:Q9SNV3; EMBL;AJ011623; PIDN:CAB56570.1
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Pred. No. 17;
0; Mismatches 6; Indels
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37.5%; Score 46.5; Di
Best Local Similarity 40.9%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative (
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Search completed: November 10, 2004, 14:52:16 Job time : 5.39623 secs
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
Accession: H83737
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C;Species: Bacillus halodurans
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                                                                                                 DB 2; Length 632;
55;
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                                                                                                                                                                                                               2; Indels
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1 Similarity 58.8%;
10; Conservative
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289 EPIADLIRKKRDRPS 303
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KPIADLYRGRESRPS 19
                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
A;Gene: TP0413
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RESULT 15 JC2369 ribosomal protein L15, cytosolic [validated] - rat

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A;Accession: JC2369
A;Molecule type: mRNA
A;Residues: 1-204 <CHA>
A;Cross.references: UNIPROT:P61314; EMBL:X78167; NID:g515864; PIDN:CAAS5026.1; PID:g515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AjGene: L15
C;Superfamily: rat ribosomal protein L15
C;Superfamily: rat ribosomal protein L15
F;2-204/Product: ribosomal protein L15 #status experimental cMAT>
F;2-204/Product: myloid hexapeptide TYKFFE motif
F;126-131/Region: amyloid hexapeptide TYKFFE motif
F;126-131/Region: nucleotide-binding motif A (P-loop)
F;126-131/Region: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
C;Species: Rattus norvegicus (Norway rat)
C;Dates: 21-Jul-2000 #sequence revision 21-Jul-2000 #text_change 09-Jul-2004
C;Datession: 402239; F22233; F22236; F22158
R;Chan, Y: L; Olvera, J; Wool, I.G.
Biochem, Biophys. Res. Commun. 201, 108-114, 1994
A;Title: The primary structure of rat ribosomal protein 115.
A;Reference number: JC2236; MUID:94256965; PMID:8198562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 2-26,137-173 <CH2>
A;Experimental source: liver
A;Note: the protein is designated as ribosomal protein L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45.5; DB; Pred. No. 19; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WOYKPIADLYRG-RESRPSAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
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us-10-092-750-47.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:38:57; Search time 29.3057 Seconds (without alignments) 431.938 Million cell updates/sec Run on:

US-10-092-750-47 124 1 PWQYKPIADLYRGRESRPSAPR 22 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of result's predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9ye21 aeropyrum p	fremyel			Q8ppg8 xanthomonas		80		Q6jin2 bovine papu	synecho	Q6tva9 bovine papu	e				Q82bhl streptomyce	4	~	Q9cy74 mus musculu	homo	mus n	Q6zue3 homo sapien	œ		Q96lw4 homo sapien	Aah64600 homo sapi	Q8chd2 mus musculu	094872 homo sapien	4	'n	~
ID	, ≽	Фено16	Q7ZXX1	Q9N883	BETA XANAC	Q8VW43	Q6L420	AAT39963	Q6JIN2	P72766	Q6TVA9	AAR98436	Q7Q7A9	-Q9ZVH6	Q9M0T7	Q82BH1	Q8H8M4	Q9S9Y3	Q9CY74	Q8N5E2	Q7TPP7	Q6ZUB3	BAC86282	BETA XANCP	Q961W4	AAH64600	Q8CHD2	094872	Q8A3U4	Q7T3P3	RL15_CHITE
DB	i N	~	~	N	~	~	~	~	~	~	N	7	~	~	~	~	~	~1	~	~	7	N	~	Н	7	~	~	N	~	~	П
Length		211	394	458	556	1017	1483	1483	163	488	683	683	197	217	282	441	637	747	152	348	348	364	364	LO.	260	260	н	φ	33	m	0
ਨਿਚ	43.5	41.9	41.9	41.1	41.1	41.1	41.1	41.1	40.7	40.7	40.7	40.7	40.3	40.3	40.3		40.3	ö	39.5	ę,	٠	39.5	6	٠	•	39.5	e,		•	φ.	39.1
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P61367 epinephelus Q7t3n2 monopterus Q7t3n9 sinipperca k Q6t278 acipenser g Q6t279 acipenser s Q6t279 acipenser s A859857 acipenser A859858 acipenser A859858 acipenser A859858 acipenser Q891m6 anaplasma o Q19746 caenorhabdi Q77459 neurospora Q75641 neurospora Cae85584 neurospora
RL15_EPICO RL15_MONAL RL15_MONAL RL15_SINKN 06T279 06T279 06T280 0AS59859 AAS59859 AAS59859 AAS59859 AAS59866 INX3_CAEEL INX3_CAEEL O7KW59 07KW59 07KW59
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203 203 2003 2003 2004 2004 2004 1223 1225 1225
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ALIGNMENTS

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Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO444084; AAH44084.1; -.
HSSP; P13590; 11ES.
                                                                                                                                                                                                                                              PEGN; PF00047; 19; 3.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IG25; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 394 AA; 42730 MW; F1141D8E6B69254A CRC64;
                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
                          FROM N.A.
[3]
SEQUENCE FROM N
TISSUE=Embryo;
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OBPPG8;
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BETA XANAC
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Necll-pending-prov protein.

Enderis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
Stowe-Evans E.L., Ford J., Kehoe D.M.; "Genomic DNA Microarray Analysis: Identification of New Genes Regulated by Light Color in the Cyanobacterium Fremyella
                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.9%; Score 52; DB 2; Length 211;
47.6%; Pred. No. 14;
iive 3; Mismatches 8; Indels
                                                                                                                                                                                             Stower Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 78548456; AAT41953.1; -.
InterPro; IPR00253; FHA.
InterPro; IPR00253; FHA.
FAR.
FAR.
FRO0498; FHA; 1.
PEGMT; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SEQUENCE 211 AA; 23789 MW; D9FD3D51813EC871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;

    Bacteriol. 186:4338-4349 (2004).

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Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.63
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                           STRAIN=FD33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q7ZXX1
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Gaps
                                                               Gaps
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Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,
del Portillo H.A., Lanzer M., Barrell B.G., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL360354; CAB96715.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
Gal Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium vivax.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5855,
Query Match 41.9%; Score 52; DB 2; Length 394; Best Local Similarity 60.0%; Pred. No. 27; Matches 12; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0%; Pred. No. 45;
Matches 8; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 AA; 53134 MW; 785060C82705BB16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Vir28 protein.
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29-MAR-2004 (Rel. 43, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Cholina dehydrogenase (EC 1.1.99.1) (CHD) (CDH).
Name=betA, OrderedLocusNames=XACQ718;
                                                                                                                                                                                                                                                                                                                                    458 AA.
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                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                           225 OYKPTAKI----ESRPSMPR 240
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                                                                                                                        3 OYKPIADLYRGRESRPSAPR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 WOYKPIADLYRGRESRPSAP 21
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                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                        M. GO, GO.0003842; F:1-pyrroline-5-carboxylate dehydrogenase act...;

RO, GO.0003842; F:1-pyrroline-5-carboxylate dehydrogenase act...;

RO, GO.0016491; F:DNA binding; IEA.

RO, GO.0016491; F:proline dehydrogenase activity; IEA.

RO, GO.0016564; F:pranscriptional repressor activity; IEA.

RO, GO.0016564; F:pranscriptional repressor activity; IEA.

RO, GO.0008152; P:metadolism; IEA.

RO, GO.0008152; P:metadolism; IEA.

RO, GO.0006562; P:proline catabolism; IEA.

RO, GO.0006562; P:proline catabolism; IEA.

RICEPPO; IPR0012850; Bifunct_PutA.

RICEPPO; IPR0012850; Bifunct_PutA.

RICEPPO; IPR001287; Pro_dh; 1.

REPROSITE; PEOSONO; Bifunct_PutA; 1.

RESP: PIREFO0017; Aldedh; 1.

REPROSITE; PEOSONO; Bifunct_PutA; 1.

ROSSITE; PEOSONO; Bifunct_PutA; 1.

ROSSITE; PEOSONO; Bifunct_PutA; 1.

ROSSITE; PEOSONO; BILDINED EHYDR.

RESPONDING; BILDINED EHYDR.

RESPUENCE 1017 AA; 111471 MW; EAB350BOB4EA5ASB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC146506; AAT19963.1; -
InterPro; IPR009023; BlueCu 1.
InterPro; IPR009007; Pept_Aspartic.
InterPro; IPR009047; Rve.
InterPro; IPR00047; Rve.
Pfam; PF00065; rve; 1.
Pfam; PF00078; RVT; 1.
PROSTIE; PS00196; COPPER BLUB; UNKNOWN 1.
POLYPEOTEIN; RNA-directed DNA polymeraes; Transferase.
SEQUENCE 1483 AA; 169333 MM; 30D527FF57244348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Buell R.C., Liu J., Zaborsky J., Tallon L., Baker B.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 2; Le:
Pred. No. 1.1e+02;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526 RPTADRRQGRDSRPQAHR 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KPIADLYRGRESRPSAPR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum demissum (Wild potato)
                     EMBL; AF306633; AAL35755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.1%;
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C
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Name=PGEC989P08.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell R.;
Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q6L420;
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ID Q6
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RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Clearelli R.M.B., Coutinho L.D., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Esuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.M., Martinac-Rossi N.M.,
Martins E.C., Machado M.J., Madeira A.M.B.M., Martinac-Rossi N.M.,
Martins E.C., Machado M.J., Madeira A.M.B.M., Miyaki C.Y., Moon D.H.,
Noreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
R. Spinola L.A.F., Takita M.A., Famura R.E., Teixeira B.C., Tezza R.I.D.,
Thindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
R. Schubal J.C., Kitajima J.P.;
R. Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: Can catalyze the oxidation of choline to betaine aldehyde and betaine aldehyde to glycine betaine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bradyřhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      reduced acceptor.
--- COFACTOR: FAD (By similarity).
--- PATHWAY: Betaine biosynthesis from choline; first step.
--- SIMILARITY: Belongs to the GMC oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 62.5%; Pred. No. 55;
Conservative 1; Mirmarchon
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InterPro; IPR00172; GMC_oxred.

InterPro; IPR07867; GMC_oxred_C;

Pfam; PF0732; GMC_oxred_T; 1.

PROSITE; PS00623; GMC_oxred_N; 1.

TIGRRAMS; TIGR01810; betA; 1.

PROSITE; PS00624; GMC_OXRED_1; 1.

PROSITE; PS00624; GMC_OXRED_2; 1.

Complete proteome; FAD; Flaroprotein; Oxidoreductase.

NP_BIND

6 35 FAD (ADP part) (Probable).
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Wu B., Tang X., Bai X., Tang D., Lu A., Tang J., Ma Q.;
Submitted (EEP-2000) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556 AA; 61265 MW;
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                                                                                                                                                                                                                                                                                                                                                                 Nature 417:459-463 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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ACT SITE SEQUENCE

SOTT THE WARRANT TO COUNTY TO THE PROPERTY OF THE PROPERTY OF

Query Match Local

Best Loc Matches

Name=putA;

Q8VW43; QBVW43

RESULT 6

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Gaps

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4; Indels

Length 163;

DB 2;

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163 AA; 17939 MW; 1630AB5779679861 CRC64;
                                                                                                                                               40.7%; Score 50.5; I 61.1%; Pred. No. 17; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     PWLYDPMSALSRGARESR 74
                                                                                                                                                                                                                                                                                                   17
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EMBL; D90900; BAA16781.1; -.

PIR; 874629; 874629.

Complete proteome.
                                                                                                                                                                                      ilarity 61.1%;
Conservative
EMBL; AY453689; AAS13365.1;
NON_TER 1
                                                                                                                                                                                                                                                                                               1 PWOYKPIADLYRG-RESR
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                          Local Similarity
tes 11; Conserv
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NCBI_TaxID=129727;
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01-FEB-1997
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                                                                             SEQUENCE
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QGTVA9
1D QGTVA
AC QGTVA
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-JU
DE ORFOT
OC VITUS
OC VITUS
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Matches
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           STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solanum demissum (Wild potato).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Spermatos, Solanales; Solanacees; Solanum.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative viral core protein P4b (Fragment).
Bovine papular stomatitis virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
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                                                  4; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC146506; AAT39963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Buell R.C., Liu J., Zaborsky J., Tallon L., Baker B.;

"Solanum denisum chromosome 5 BAC PGEC989P08 genomic se
submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 1.6e+02;
               Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                             PRT; 1483 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%;
illarity 46.7%;
Conservative
               46.78;
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75 PWKYEPTVVTYKGKE 89
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                                                                                                                                                                   1 PWOYKPIADLYRGRE
                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative polyprotein. PGEC989P08.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ronning C.M.;
Submitted (AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2004)
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nes 7; Conserv
           Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=50514;
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                                                                                                                                                                                                                                                                                                                                                                                 AAT39963
AAT39963;
01-JUN-2004
01-JUN-2004
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SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6JIN2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
0RF079 virion core protein 44b.
Bovine papular stomatitis virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINES 2012753, PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence analysis of the genome of the genome features in the 1 Mb
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 AA; 57146 MW; 578A0B158BE99766 CRC64;
                                                                                                                                                                            Sll1686 protein.
Ordered.cousNames=sll1686;
Synechocystis sp. (strain PCC 6803).
Bacteris sp. Cyanobacteria; Chrococcales; Synechocystis.
                                                               (Trimblrel. 02, Created)
(Trimblrel. 02, Last sequence update)
(Trimblrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 AA.
488 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PCC6803;
MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PWQYKPIADLYRGRESRP 18
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Gaps

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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-AT4907710;
Name-AT4907710;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shounsley S.D., Fraser C.M., Somerville C.R., Venter J.C.;
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
STRAIN=PEST;
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
LCAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL; AAABO1008960; EAA11143.1; -.
SEQUENCE 197 AA; 22589 WW; BB877FB775441505 CRC64;
                                                                                                                                                                                Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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SEQUENCE FROM N.A.

Town C.D., Kaul S.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AC005499; AAC67366.1; -.

PIR; A484806; AA84906.

InterPro; IPR005162; Retrotrans gag.

Pfam; PF03732; Retrotrans gag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                            Score 50; DB 2;
Pred. No. 25;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 2
Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative retroelement pol polyprotein.
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                                                                                                                                                                                                                                                                                  7 KPIRVDRYQGRESIFKRPNAP 27
                                                                                                                                                                                                                                                         5 KPI-ADLYRGRES---RPSAP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 PEDYKPIVDOMEGRDTPPN 196
                                                                                                                                                                            Query Match
Best Local Similarity 61.9%; Pre
Matches 13; Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
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                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=At2g38520
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Q9ZVH6
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Q9MOT7
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                                                                      Delhon G., Tulman B.R., Afonso C.L., In Z.,
de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.B., Kutish G.F.,
Rock D.L.,
"Genomes of the Parapoxviruses Orf Virus and Bovine Papular
Stomtatitis Virus.",
J. Virol. 78:168-177 (2004).
EMBL; AX386265, AR48436.1; -.
InterPro; IPR004972; Pox P4B.
Pfam; PF03292; Pox P4B; I.
SEQUENCE 683 AA; 74507 MW; OFA9C718677BBE48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BV-AR02;
PubMed=14671098;
Delhon G., Tulman E.R., Afonso C.L., Iu Z.,
de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine papular stomātitis virus.
Viruses, daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
NCSI_TaxID=129727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomes of the Parapoxviruses Orf Virus and Bovine Papular Stomtatilis Virus.";
J. Virol. 78:168-177(2004).
EMBL; AY386265; AAR98436.1; -
SEQUENCE 683 AA, 74507 MW; 0FA9C718677BBE48 CRC64;
                                                                                                                                                                                                                                                                                                                                      Indels
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2004 (TrEWBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
0RF079 virion core protein P4b.
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                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  683 AA.
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.1%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.7%; Score 50.5; D
Best Local Similarity 61.1%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                              577 PWLYDPMSALSRGARESR 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                      PubMed=14671098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004
01-MAR-2004
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AAR98436

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Gaps

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RESULT 13

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RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

BR EMBL; Ali61507; CAB77930.1; -.

DR PIR; A85076; A85076.

KW Hypothetical protein.

SQ SEQUENCE 282 AA; 31518 MW; 1A691C1C95991A03 CRC64;

Query Match

40.3%; Score 50; DB 2; Length 282;

Best Local Similarity 60.0%; Pred. No. 37;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 10, 2004, 14:50:04 Job time : 31.3057 secs

5 KPIADLYRGRESRPS 19 :|||||:| 188 EPIADLFRKKRERPS 202

8 8

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Sequence 2 Sequence 4 Sequence 6

Sequence Sequence Sequence

Sequence

Sequence

Sequence 3 Sequence 4 Sequence 6 Sequence 8 Sequence 1

Sequence Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: GONZALEZ Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIVET4 AND CIVET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSER: Nadel
ADDRESSER: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FLIANG DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EGGL' CHRISTOPHE:
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECHOME: Z15-75-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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61.5%; Pred. No. 20;
cive 4; Mismatches
US-08-980-071-10
US-08-980-071-59
US-08-980-071-59
US-08-757-536-4
US-08-757-536-4
US-08-757-536-6
US-08-757-536-10
US-08-757-536-10
US-08-757-536-10
US-08-757-536-10
US-09-314-093-4
US-09-314-093-6
US-09-314-093-6
US-09-314-093-8
US-09-314-093-8
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US-09-314-093-10
US-09-314-093-10
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US-09-314-093-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08100709 Patent No. 5322687
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Best Local Similarity 61.5
Matches 8; Conservative
                       ; MOLECULE TYPE: protein US-08-100-709-2
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LLQFLLNNFVPGG
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   TOPOLOGY:
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 12404, A
Sequence 2, Appli
Sequence 11, Appli
                                                                                                                          November 10, 2004, 13:44:14 ; Search time 6.58868 Seconds (without alignments) 181.178 Million cell updates/sec
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Sequence 21
Sequence 16
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Sequence
Sequence
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'GGTZ_6/ptodata//iaa/5A_COMB.pep:*
'GGTZ_6/ptodata/1/iaa/6A_COMB.pep:*
'GGTZ_6/ptodata/1/iaa/6A_COMB.pep:*
'GGTZ_6/ptodata/1/iaa/6A_COMB.pep:*
'GGTZ_6/ptodata/1/iaa/PCTUS_COMB.pep:*
'GGTZ_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   5.1.6
Compugen Ltd.
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US-08-176-865-2
US-08-176-865-2
US-08-176-096-2
US-08-179-046-2
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US-08-179-046-2
US-08-961-803-8
US-08-961-803-8
US-08-961-805-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-9867-2
US-08-71-986-16
US-08-71-986-16
US-08-71-986-16
US-08-980-071-4
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US-08-980-071-4
US-08-980-071-4
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                                                                                                                                                                                                                                                                                                                                       478139 seqs, 66318000 residues
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                   GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                    US-10-092-750-48
91
1 LFSVLLRYLADNFLPGGS 18
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Indels

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Sequence 2, Application US/08474038

Pareant No. 5673943

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Jan, Yubing
APPLICANT: Jan, Yubing
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
                      Sequence 2, Application US/08176865

Patent No. 5615319

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Josee M.
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
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                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nadel
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: US/08/176,865
FILING DATE: 29-ULL-1993
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27633
REPRENCE/DOCKET NUMBER: 2763
RELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TWDE. amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1
Pred. No. 20;
4; Mismatches
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41 LLOFLLNNFVPGG 53
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Best Local Similarity 61.5
Matches 8; Conservative
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TOPOLOGY: linear
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RESULT 2
US-08-176-865-2
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COMPUTER FEOREM.

WENDING TYPE: FORDER FORM:
WENDING SEPERATURED WITH FORDER FORM:
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Pred. No. 20;
4; Mismatches 1; Indels
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US-08-961-803-8
i. Sequence 8. Application US/08961803
i. Patent No. 6150589
i. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            52.7%;
61.5%;
        41 LLQFLLNNFVPGG 53
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Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-08-448-170-6
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                                                                                                  Score 48; DB 2; Length 1167;
Pred. No. 20;
                                                                                                                  1; Indels
                                                                                                                   4; Mismatches
                   REFERENCE/DOCKET NUMBER: 7205
TELECOWINICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acids
       NAME: Egolf, Christopher REGISTRATION NUMBER: 27633
                                                                                                   52.7%;
ATTORNEY/AGENT INFORMATION
                                                                                                                                5 LLRYLADNFLPGG 17
                                                                                                                                         ||::| :||:||41 LLQFLLNNFVPGG 53
                                                                                                                  8; Conservative
                                                                     ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-779-046-2
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MOLECULE TYPE: protein
                                                                                                   Query Match
Best Local Similarity
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US-08-881-340-2
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Patent No. 5336623
GENERAL INFORMATION:
APPLICANT: VON TERSCH, Michael A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYETI TOXIN GENE TITLE OF INVENTION: AND PROTEIN TOXIC TO LEPIDOPTERAN INSECTS NUMBER OF SEQUENCES:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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pred. No. 20;
4; Mismatches 1; Indels
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Pred. No. 20;
4; Mismatches 1; Indels
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ADDRESSE:
ADDRESSE:
CITY:
Philadelphia
STARE:
Philadelphia
STARE:
STARE:
COUNTRY:
U.S.A.
ZIP:
19103
COMPUTER READABLE FORM:
MEDIUM TYPE:
FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE:
FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE:
FORM:
COMPUTER PARTIN PC-DOS/MS-DOS
SOFTWARE:
FORM:
APPLICATION NUWBER:
CLASSIFICATION NUWBER:
FILING DATE:
FLING DATE:
APPLICATION NUWBER:
CLASSIFICATION NUWBER:
TELECOMMUNICATION:
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; TITLE OF INVENTION: and Methods of Use; FILE REFERENCE: MECO201; CURRENT APPLICATION NUMBER: US/09/661,322A; CURRENT FILING DATE: 2000-09-13; NUMBER OF SEQ ID NOS: 63; SOFTWARE: Patentin version 3.0; SOFTWARE: Patentin version 3.0; SOFTWARE: PRT TYPE: FRT TYPE: FRT US-09-661-322A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-12404
; Sequence 12404, Application US/09489039A
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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41 LLQFLLNNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-032-364-2
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Sequence 22, Application US/09661322A

Sequence 22, Application US/0966132A

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
                                                             APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PSISSC2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
TOWNERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMPPY disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 13-SEPT-1991
CLASSIFICATION BOTA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 33-MAY-1995
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 33-MAY-1995
CLASSIFICATION NUMBER: W/S 102DCD1
TELEBRENCE/DOCKET NUMBER: M/S 102DCD1
TELEBRANCE/COCKET NUMBER: M/S 102DCD1
TELEBRANCE/COCKET NUMBER: M/S 102DCD1
TELEBRANCE (352) 375-8800
INFORMATION FOR SQ 1D0 OS
SEQUENCE: CRARACTERISTICS:
L'ENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galnesville
STATE: Florida
                                Payne, Jewel
Cummings, David A.
Cannon, Raymond J.C.
Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LLRYLADNFLPGG 17
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-961-803-8
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Gaps

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Indels

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Mismatches

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7; Conservative
Matches
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       GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT PELLOATION NUMBER: US 60/117,747
PRIOR PELLOATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12404
LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 2, Application US/08771986A

Batent No. 6043415
GENERAL INFORMATION:
APPLICANT: STRIZHOV, Nicolai
APPLICANT: SCHELL, Jeff
APPLICANT: ZILBERTSTEIN
APPLICANT: SCHELL, Jeff
APPLICANT: SCHELL, Jeff
APPLICANT: SCHELL, Jeff
APPLICANT: SCHELL, Cacha
TITLE OF INVENTION: SYNTHETIC BACILLUS THURINGIENSIS GENE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 4; Length 696;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUMPLAIL: CUST.

ZIF: ZOOUT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Tab PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PacentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,986A
FILING DATE: 23-DEC-1996
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: PEET, Richard C.
REGELSTRATION NUMBER: 35,792
REFERENCE/DOCKET NUMBER: 026433/0118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 3;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 FPVSLRISADDFLKGGN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FSVLLRYLADNFLPGGS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                  50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 630 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.8<sup>1</sup>
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 630 amino act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-771-986A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-771-986A-2
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ORGANISM: SOLUTION CONCERNIAL SOLUTION CONCERNISM: R26-21 MR1-37, subsp. aizawai 7.29
INDIVIDUAL ISOLATE: not applicable
TISSUE TYPE: not applicable
TISSUE TYPE: unicellular organism
TWEDIATE SOURCE: strains K26-21, MR1-37, subsp. aizawai
TWEDIATE SOURCE: 7.29
INMEDIATE SOURCE: 7.29
INMEDIATE: not applicable
POSITION IN GENOME: not applicable
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
NAME/KEX: solution in a proprietable
NAME/KEX: solution in a proprietable
NAME/KEX: relevant residues from 1 to 630
INCATION METHOD: by experiment
INCATION METHOD: by experiment
OTHER INFORMATION: genus confers Spodoptera resistance being expressed in trans
                                                                                                                                                                                       Sequence 2, Application US/08769802A
Patent No. 6110668
CENERAL INFORMATION:
APPLICANT: Strizhov, Nicolai; Koncz, Csaba; Schell, Jeff
TITLE OF INVENTION: Gene Synthesis Method
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADGRESSE: ADGRESSE: ADGRESSE: 900 17th Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage COMPUTER: IEM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/769,802A
FILING DATE: 20 - DEC - 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,896
FILING DATE: 07 - OCT - 1996
ATTONEY/AGENT INFORMATION:
NAME: COAGN, HERDET
REGISTRATION NUMBER: 25,109
REPERECAMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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LENGTH: 630 amino acid residues
TYPE: amino acid acid residues
TOPOLOGY: linear
MOLECULE TYPE:

DESCRIPTION: truncated protein
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal fragment
5 LLRYLADNFLPGG 17
                                    41 LVQFLVSNFVPGG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 900 17th
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: no
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                       RESULT 12
US-08-769-802A-2
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APPLICANT: SANCHIS, Vincent
MENDU, Ghislaine
MENDU, Ghislaine
MENDU, Ghislaine
MARTOURET, Daniel
DEDONDER, RAYMOND
TITLE OF INVENTION: NUCLEOTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1; Length 823;
Pred. No. 42;
4; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
   COMPUTER READABLE FURM:
MEDIUM TYPE: Ridby disk
COMPUTER: IBM PC compatible
COMPTUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
FRIOR APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
FRICK APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 10-DEC-1989
FRICK APPLICATION NUMBER: FR 97 08090
FILING DATE: 10-UN-1987
FILING BATE: 10-UN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STRET: P.O. Box 1404
CITA Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEPIDOPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09037621A
Patent No. 6310035
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LLRYLADNFLPGG 17
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41 LVQFLVSNFVPGG 53
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-037-621A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-461-551-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8103, Application US/09328352
Patent No. 6562946
STREAT INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: GT-09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8203
LENGTH: 773
OTHER INFORMATION: plants
PUBLICATION INFORMATION:
AUTHORS: Strizhov, Nicolai, Keller, Menachem; Mathur, Jadeep;
AUTHORS: Strizhov, Nicolai, Keller, Menachem; Mathur, Jadeep;
AUTHORS: Koncz.ko lm n. Zsuzaana; Bosch, Dirk; Prudovsky, Evgenia; Schell, AUTHORS: Jeff; Sneh, Baruch; Koncz, Csaba; Zilberstein, Aviah
TITLE: A synthetic cryIC gene, encoding a Bacillus thuringiensis
TITLE: A synthetic cryIC gene, encoding a Bacillus thuringiensis
UOURNAL: Proc. Natl. Acad. Sci. USA
ISSUE: 29
ISSUE: 28
PAGES: 15012 - 15017
DATE: 24 - DEC - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCES CODING FOR POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS LEPIDOPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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49.5%; Score 45; DB 4; Length 773;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 10; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 3; Length 630;
Pred. No. 31;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08461551
; Sequence 2, Application US/08461551
; Patent No. 579298
; GENERAL INFORMATION:
APPLICANT: LERECLUS, Didier
APPLICANT: LERECLUS, Didier
APPLICANT: MARTOURET, Marguerite-Marie
APPLICANT: MARTOURET, Daniel
APPLICANT: MARTOURET, Daniel
APPLICANT: MARTOURET, Daniel
APPLICANT: MARTOURET, Daniel
APPLICANT: MARTOURES, Raymond
TITLE OF INVENTION: POLYPEPTIDES ENDOWED WITH
TITLE OF INVENTION: LEPIDOPTERA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: PO. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Acinetobacter baumannii
US-09-328-352-8203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1||| || || 1|
261 LFSVFLRMLDENALP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LFSVLLRYLADNFLP 15
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COUNTRY: USA
ZIP: 22313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-328-352-8203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-461-551-2
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Gaps ..

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us-10-092-750-48.rai
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Query Match 49.5%; Score 45; DB 3; Length 823; Best Local Similarity 53.8%; Pred. No. 42; Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/461,551
FILING DATE: -CURROWN:
APPLICATION NUMBER: US 07/458,754
FILING DATE: 10-DEC-1899
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 10-UNJ-1987
ATTORNEY/AGETY INFORMATION:
NAME: HUNTINGTON, R. D.
REFIERPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPAX: (703) 836-2021
TELEFAX: (703) 836-6620
TELEMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
TERMANDENNESS: unknown
SEQUENCE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-037-621A-2

49.5%; SCOFE 45; DB
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,621A
FILING DATE: 10-MAZ-1998
CLASSIFICATION: <UNKNOWN>
11-DEC-1989
06-MAY-1988
10-JUN-1987
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Search completed: November 10, 2004, 14:55:36 Job time : 7.63868 secs

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US-10-102-469-20

US-10-200-522-2

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             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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1 LFSVLLRYLADNFLPGGS 18
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seq length: 200000000
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Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Sequence 48, Appl
Sequence 22, Appl
Sequence 4, Appli
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Sequence 273457,
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Sequence 72803, A
Sequence 147749,
Sequence 2, Appli
Sequence 2, Appli
Sequence 21, Appli
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                 1 US-10-092-750-48

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2 US-10-428-961-22

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6 US-10-437-95-3173457

7 US-10-425-115-29841

5 US-10-425-114-60096

5 US-10-425-114-60096

5 US-10-425-114-60096

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6 US-09-118-4599-147749

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REBULT 1
US-10-092-750-48

i Sequence 48, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
    APPLICANT: Hammond, Philip W.
    APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
    TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFRENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR PILING DATE: 2001-06.08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 48

LENGTH: 18
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100.0%; Pred. No. 7.4e-08;
cive 0; Mismatches 0;
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Sequence 22, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-10-092-750-48
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Score 46; DB
Pred. No. 11;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
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APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Glonovan, William P.

APPLICANT: Glonovan, William P.

APPLICANT: Glonovan, William P.

APPLICANT: Glonovan, William P.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFRENCE: MECO201-1,

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2000-09-13

FRIOR PRILOR APPLICATION NUMBER: 60/1322

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 22

**ENOTH: 168

**CHARTH: Light Application Number OF SEQ ID NO 2.2

**ENOTH: Light Application Norsion 3.2

**ENOTH: Light Application Norsion 3.2
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JOSTICA DATE: 2004-04

JOSTICA DATE: 2004-016020A1

JOSTICANT: SPERIAL INFORMATION:

APPLICANT: Arnaut, Greta

APPLICANT: Damme, Nicole

APPLICANT: Wanneste, Stijn

APPLICANT: Vanneste, Stijn

FILE REFERENCE: NEWETSUS2

CURRENT APPLICATION NUMBER: US/09/739,243

PRIOR APPLICATION NUMBER: 60/173387

PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 4

LENGTH: 1168
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Pred. No. 76;
4; Mismatches 1; Indels
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Pred. No.
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Publication No. US/20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Bacillus thuringiensis US-10-614-524-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Bacillus thuringiensis US-10-428-961-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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US-10-425-115-281976
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Can Rosa, Thomas J.
APPLICANT: Exceler, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: APPLICANT: All Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174457
LENGTH: 318
Page 2

APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 281976
LENGTH: 97
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Publication No. US20040214272A1
GENERAL INPORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yahua
APPLICANT: Zhou, Yahua
APPLICANT: Chou, Yahua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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US-10-437-963-173457
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OTHER INFORMATION: Clone ID: MRT4577_20262C.1.pep
US-10-425-115-281976
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TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Zea mays
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JOHNSON TO
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| Publication No. US200400348881|
| Publication No. US200400348881|
| GENERAL INFORMATION: | APPLICANT: Liu, Jingdong | APPLICANT: Liu, Jingdong | APPLICANT: Edou, Yihua | APPLICANT: Screen, Steven E | APPLICANT: Tabaska, Jack E | APPLICANT: Tabaska, Jack E | APPLICANT: Cao, Yongwei | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: NUMBER: US/10/425,114 | CURRENT FILING DATE: 2003-04-28 | NUMBER OF SEQ ID NOS: 73128 | SEQ ID NOS: 73487 | SEQ ID NOS: 73128 | SEQ ID NOS: 73487 | SEQ ID NOS: 73484 | SEQ ID NOS: 73487 | SEQ ID NOS: 73484 | SEQ ID NOS: 73487 | SEQ ID NOS: 73484 | SEQ ID 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 17; Length 619;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Clone ID: LIB3593-007-E1_FLI.pep
US-10-425-114-37487
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANIEM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_168593C.1.pep
US-10-425-115-259841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.9%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 259841
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 LLSGILLYLGSTYLPGG 116
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-10-425-114-37487
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Sequence 147749, Application US/10424599;
Sequence 147749, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwin K
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-72803

VS-10-425-114-72803

Sequence 72803, Application US/10425114

Fublication No. US20040034888A1

Fublication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwai

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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50.5%; Soore 46; DB 15; Length 622;
Best Local Similarity 52.9%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 6; Indels
TYPE: PRT | ORGANISM: Zea mays | FEATURE: | PRATURE: | OTHER INFORMATION: Clone ID: LIB3632-026-F12_F1I.pep US-10-425-114-60096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: LIB4702-003-B5_FLI.pep
US-10-425-114-72803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
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Fri Nov 12 14:55:32 2004

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Query Match

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APPLICANT: Gardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT PLING DAPE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR PILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 21
LENGHAL: 1163
                      Gaps
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Publication No. US20030101482A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GILMER, Amy Jelen
Mettue, Anna-Narie Light
Mettue, Anna-Narie Light
ITLE OF INVENTION: TEARANET FLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 9; Length lle. Pred; No. 2.38+02; 2; Indels
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-21
  Pred. No. 1.6e+02;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                Sequence 21, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 4433
    53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.5%;
ilarity 53.8%;
Conservative
                                                                 5 LLRYLADNFLPGG 17
                                                                                               41 LVQFLVSNFVPGG 53
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                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
Best Local Similarity
Matches 7; Conserv
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Publication No. US20030115628A1
GENERAL INPORMATION:
APPLICANT: SANCHIS, Vincent
LERECLUS, Didier
MENOU, Ghislaine
LECADET, Marguerite-Marie
DEDONDER, Raymond
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
LEPIDOPTERA
LEPIDOPTERA
                                                                                                                                   ö
                                                                                                                                     Gaps
                                                                                                                                   ;
0
                                                                                          Length 71;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
      ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104438C.1.pep
US-10-424-599-147749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS.
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                        Score 45; DB 15;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/918,485
FILING DATE: 25-001
CLASSIPICATION: <UNKNOWN-
PRIOR APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-UN-1995
FILING DATE: 05-UN-1995
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: ER 8401 121.4
FILING DATE: 10-UN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REFERENCE/DOCKET NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 27,903
                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
;
MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-918-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 823 amino acids
                                                                                        Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                              6 LRYLADNFLPGGS 18
                                                                                                                                                                                                                   16 LSHLADHFLPWGS 28
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US-09-918-485-2
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Gaps
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3-8-01-75-6
5-09-972-175-6
Sequence 6, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baun, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
Mettus, Anne-Marie Light
IITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 10; Length 1189;
Pred. No. 2.46+02;
4; Mismatches 2; Indels
    Length 1189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/337,635
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                Indels
Query Match
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 11, 2004, 02:43:04 Job time: 21.8689 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ' TOPOLOGY: linear

) MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-972-175-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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41 LVQFLVSNFVPGG 53
                                                                                             5 LLRYLADNFLPGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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Sequence 4, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSCENIC PLANTS EXPRESSING
                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 10; Length 1189;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TO SEQUENCES: A
NUMBER OF SEQUENCES: A
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/972,175
FLING DATE: 05-06-1201
CLASSIFICATION NUMBER: 09/337,635
FLING DATE: CLUKNOWN:
APPLICATION NUMBER: 09/337,635
FLING DATE: CLUKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BADABLE SI 928
REGISTRATION NUMBER: 33,928
REPERENCE/DOCKET NUMBER: BECO: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                     NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERRENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-972-175-4
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
       APPLICATION NUMBER: 09/337,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 512/418-3000
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                            FILING DATE: <Unknown ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S LLRYLADNFLPGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::| ||:|||
41 LVQFLVSNFVPGG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                             TYPE: amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-972-175-4
                                                                                                                                                                                                                                                                                                                                                                    US-09-972-175-2
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-48 '91 1 LFSVLLRYLADNFLPGGS 18 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Libting first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

ATP-dependent CLP	hypothetical prote	endopeptidase Clp	endopeptidase Clp	probable pre-tRNA	nad-specific gluta	parasporal crystal	multidrug resistan	BIR repeat contain	cutinase - fungus	sensor histidine k	hypothetical prote	glucose-1-phosphat	O-antigen polymera	glycerol trinitrat	hypothetical prote
F81396	C87358	AC2096	1060NC	T40803	T40931	A48970	T18279	T31067	821427	H87561	G72778	T48866	A47677	AI3558	T26511
7	0	~	N	N	N	N	N	N	-	N	(7	N	~	~	0
857	859	880	945	978	1106	1176	1743	4845	223	839	138	355	359	371	378
45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	44.5	44.5	44.0	44.0	44.0	44.0	44.0
41	41	41	41	41	41	41	41	41	40.5	40.5	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AB1136	
NADH flavin oxidoreductase homolog lmo0489 [imported] - Listeria monocytogenes (strain	nes (strain
C;Species: Listeria monocytogenes	
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C;Accession: AB1136	
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke	P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, 1	D.; Fsihi, P
D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; l	urnam, A.; l
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; W	H.; Wehland
A, Title: Comparative genomics of Listeria species.	
A; Reference number: AB1077; MUID:21537279; PMID:11679669	
A;Accession: AB1136	
A;Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-664 < GLA>	
A; Cross-references: UNIPROT: Q8Y9N6; GB:NC_003210; PIDN: CAC98568.1; PID:916409865; GSPDE	09865; GSPDE
A; Experimental source: strain EGD-e	
C;Genetics:	

A;Gene: 1mo0489 C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine dehydrogenase

Gaps .. 0 Ouery Match 50.5%; Score 46; DB 2; Length 664; Best Local Similarity 47.1%; Pred. No. 13; Matches 9; Conservative 4; Mismatches 5; Indels

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218 FPIVLRFSADEFTEGGN 234 2 FSVLLRYLADNFLPGGS 18 ઠે d d

RESULT 2

MDH flavin oxidoreductase homolog lin0492 [imported] - Listeria innocua (strain Clip11 C;Species: Listeria innocua innocua (strain Clip11 C;Species: Listeria innocua innocua (strain Clip12 C;Species: Listeria innocua innocua (strain C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AD194 C;Accession: AD194 C;Accession: AD194 C;Accession: AD194 C;Accession: AD194 C;Accession: AD194 C;Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeckc, J. Dominguez-Bernal, G.; Durand, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; P. Schueter, T.; Simoes, N.; Tierez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Residues: Preliminary A;Molecule type: DNA A;Residues: 1-664 <GLA> A;Residues: 1-664 <GLA> A;Cross-references: UNIPROT:092EG8; GB:ALS92022; PIDN:CAC95724.1; PID:g16412932; GSPDB

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Query Match Best Loc Matches

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A;Status: preliminary
A;Status: preliminary
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A;Status: Dred
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossides: 1-678 <KURA
A;Rossides: 1-678 <KURA
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Prinan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler
B;Galibert, F.; Prinan, T.W.; Jones, T.
Colence 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Reference number: Asgolas; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable NADH-dependent oxidase protein stcD2 [imported] - Sinorhizobium meliloti (stra C; Species: Sinorhizobium meliloti
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; File: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end A; Reference number: ASS42; NUID:21396508; PMID:11481431
                                                               Nalternate names: crylC protein
C;Species: Bacillus thuringiensis
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7140
R;Christov, N.K.; Imaishi, H.; Ohkawa, H.
Biosci: Biotechnol. Biochem. 63, 1433-1444, 1999
A;Title: Green-tissue-specific expression of a reconstructed crylC gene encoding the ptera litura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (fragment) N;Alternate names: delta-endotoxin C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
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C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine dehydrogenase
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Pred. No. 19;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 655;
                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: JC7140; MUID:99430790; PMID:10501003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 2;
Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: crylC
C,Superfamily: parasporal crystal protein
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FILGVRYTADECLPGGT 231
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-655 <CHR>
A;Cross-references: EMBL:X96682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LLRYLADNFLPGG 17
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41 LVQFLVSNFVPGG 53
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JC7140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PAB0082 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75201
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Accession: A75201
A;Reference number: A75001
A;Reference number: A75001
A;Accession: A75001
A;Accessi
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Date: 127124
R;Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamaanoto, S; Sekin
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Fudoh, Y; Yamazaki, J; Kushida, N; Oguchi
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Fudoh, Y; Yamazaki, J; Kushida, N; Oguchi
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Fudoh, Y; Yamazaki, J; Kushida, N; Oguchi
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71234
A;Accession: B71234
A;Residues: 1-570 «KMP»
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                                                                                A;Gene: lin0492
C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine dehydrogenase
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Pred. No. 16;
1; Mismatches 1; Indels
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Pred. No. 16;
1; Mismatches 1; Indels
                                                                                                                                                                                         Match
Local Similarity 47.1%; Pred. No. 13;
68 8; Conservative 4; Mismatches 5; Indels
A, Experimental source: strain Clip11262 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                     218 FPIVLRFSADEFTEGGN 234
                                                                                                                                                                                                                                                                                                                                                              2 FSVLLRYLADNFLPGGS 18
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ilarity 80.0%;
Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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211 LRYLVENFLP 220
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Best Local Similarity
Local 8; Conserva
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RESULT 5

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70513
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Reference number: A70500, MJ10:98295987; PMID:9634230
A;Reference number: A70500, MJ10:98295987; PMID:9634230
A;Retus: precliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-473 <COL.>
C;Genetics: Strain H37Rv
C;Genetics: Strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein CT764 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Ju1-2004
C;Accession: G71472
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell.
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tri
A;Reference number: A71570; MUD:99000809; PMID:9784136
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C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32647
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                      Gaps
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                      Indels
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66.7%; Pred. No. 19;
cive 0; Mismatches
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                  Mismatches
                      4;
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Best Local Similarity 66.77
Conservative
The Conservative
                                                                                  5 LLRYLADNFLPGG 17
                                                                                                                              41 LVQFLVSNFVPGG 53
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|LRFRKDSFLPG 234
                  7; Conservative
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A;Molecule type: DNA
A;Residues: 1-268 <ARN>
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tes 8; Conserv
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              Matches
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R. Sammons, L.; Wohldmann, P.
Submitted to the EMBL Data Library, July 1997
A. Description: T31742
A. Accession: T31742
A. Setreme number: Z21078
A. Setreme number: Z21078
A. Setreme preliminary; translated from GB/EMBL/DDBJ
A. Setreme: preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-1106 < SAM>
A. Cross-references: UNIPROT:016310; EMBL:AF016430; PIDN:AAB65371.1; GSPDB:GN00023; CESP:A:Experimental source: strain Bristol N2; clone C05C8
C; Accession: S04181

No. Michael S. V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.; Lecadet, M.M.

Mol. Microbiol. 3, 229-238, 1989

A; Title: Nucleotide Sequence and analysis of the N-terminal coding region of the Spodopt A; Reference number: S04181; MUD: 89343627; PMID: 2548060

A; Residence number: S04181

A; Molecule type: DNA

A; Residues: 1-823 <SAN>

A; Cross-references: UNIPROT: P05518; EMBL: X13620; NID: 940355; PIDN: CAA31951.1; PID: 940356
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R,Honee, G, van der Salm, T, visser, B.

R,Honee, G, van der Salm, T, visser, B.

A,Accession: S00944 MulD:88289380, PMID:3399402 A,Accession: S00944 MulD:88289380, PMID:399402 A,Accession: S00944 MulD:88289380, PMID:3399402 A,ACCESSION A,A
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Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CESP:COSC8.4
A;Map position: 5
A;Introns: 25/3; 78/3; 117/1; 245/1; 591/1; 787/1; 1008/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein CO5C8.4 - Caenorhabditis elegans
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Pred. No. 32;
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                          A,Gene: bta
C,Superfamily: parasporal crystal protein
C,Keywords: delta-endotoxin
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53.8%;
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1 Similarity 55.6%;
10; Conservative
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41 LVQFLVSNFVPGG 53
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Best Local Similarity 53.8
Matches 7; Conservative
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Matches 10; Conserv
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Best Local Similarity
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RESULT 9 S00944

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C;Species: Escherichia coli
C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C86128
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayne
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, S29-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: GBC128
A;Accession: GBC128
A;Accession: GBC128
A;Accession: GBC128
A;Accession: GBC128
A;Residues: 1-2113 <STO>
A;Residues: 1-2113 <STO>
A;Cross-references: UNIPROT;Q8XC71; GB;AE005174; NID:g12519309; PIDN:AAG59487.1; GSPDB:GCS-references: gtrain O157:H7, substrain BDL933
C;Genetics:
A;Gene: Z5901
                                                                                                                                                                                                                            C86128
probable helicase Z5901 [imported] - Escherichia coli (strain O157:H7, substrain EDL933
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46.7%; Score 42.5; DB 2;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 10; Conservative 2; Mismatches 1;
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1850 FALLLDYLAD---PGG 1862
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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. BNA Res. 8, 11-22, 2001
A) Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A, Reference number: A99629; MUID:21156231; PMID:11258796
A, Accession: G91286
A, Acces
             R;Lambert, B.

submitted to the EMBL Data Library, April 1993

A;Reference number: $32645

A;Accession: $32647

A;Accession: $32647

A;Acteus: preliminary

A;Residues: 1-1160 cLAM>

A;Residues: 1-1160 cLAM>

A;Residues: 1-1160 cLAM>

C;Superfamily: parasporal crystal prottein

C;Superfamily: parasporal crystal prottein

C;Keywords: delta-endotoxin
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A,Molecule type: DNA
A,Residues: 1-1165 «HOE>
A,Residues: 1-1165 «HOE>
A,Cross-tences: UNIPROT:P19415; EMBL:X54160; NID:g40279; PIDN:CAA38099.1; PID:g40280
C,Superfamily: parasporal crystal protein
C,Keywords: delta-endotoxin
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S11446
R;Hoefte, H.; Soetaert, P.; Jansens, S.; Peferoen, M.
Nucleic Acids Res. 18, 5545, 1990
A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specif
A;Reference number: S11446; MUD:91016842; PMID:2216728
A;Accession: S11446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasporal crystal protein crylDal - Bacillus thuringiensis
AlAlternate names: parasporal crystal protein crylD
C;Species: Bacillus thuringiensis
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

47.3%; Score 43; DB 2; Length 1165; Best Local Similarity 53.8%; Pred. No. 73;

Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length [160; Pred. No. 73; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::| ||:||
41 LINFLYSNFVPGG 53
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Best Local Similarity
Matches 10; Conserv
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2 FSVLLRYLADNFLPGG 17

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Gaps

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1; Indels

Length 2113;

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November 10, 2004, 13:38:57; Search time 23.9774 Seconds (without alignments) 431.938 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
                         Copyright
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1 LFSVLLRYLADNFLPGGS 18 US-10-092-750-48 91 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q6pyw6 bacillus th A893799 bacillus th Q45716 bacillus th Q25716 bacillus th Q23046 arabidopsis Q39047 arabidopsis Q3904 arabidopsis Q302az6 bacillus th Q8ptb bacillus th Q8ptb bacillus th Q7wt25 streptomyce Q7wt25 streptomyce Q7wt25 streptomyce Q70429 listeria in Q7230 listeria in Q7230 listeria mo Q7230 listeria mo Q7240 bovine herp Aar 61310 listeria Q6b12 debaryomyce Q6c242 bovine herp Aar 61310 bovine herp Q6c32 prococcus Q8v22 pyrococcus Q8v278 rhizobium m Q6fewg acinetobact Q8idf plamodium Description SUMMARIES Q39046 Q39047 C1GB_BACTZ Q8GHE8 AAS93799 C1JA_BACTU C1JB_BACTU 023678 Q6X242 AAR86131 Q6BS12 Q8H633 O57875 Q9V2E2 Q8U4L1 **292EG8** Q6FZX7 % Query Match Length DB 664 1246 1246 1250 1250 354 485 570 570 678 764 106 Score Result Š.

RHIME

STCD RH QEFEW8 Q8IDF9 O16310

P05518 bacillus th Q6ynb8 bacillus th Q91877 bacillus th	Aalroze bacillus Aalrose bacillus Q98mq3 rhizobium l Q6dfm6 xenopus tro	V/veye mycobacteri Q79fh3 mycobacteri Cae55457 mycobacte Q7q063 anopheles g	V./lw. groupacter Q94zdl eptatrecus Q8gkt8 bacillus ce
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ALIGNMENTS

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	Gaps
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IARY; PRT; 782 AA. rel. 27, Created) rel. 27, Last sequence update) rel. 27, Last sequence update) rel. 27, Last annotation rel. 27	52.7%; Score 48; DB 2; Length 782; 61.5%; Pred. No. 39; trive 4; Mismatches 1; Indels 1965 17
Created) Last sequer Last annote Fragment). Sp. kenyael) Iales, Bacil A. Shim H.J. EMBL/GenBar Xin. Xin. Xin. Xin. Xin. Xin. Xin. Xin.	17 Score 48; DB 2; Le 15 Fred. No. 39; 17 17 47 27, Created) 27, Last sequence update) 27, Last sequence update) 27, Last sequence update) 27, Last sequence update) 27, Last sequence update; 18 Subsp. kenyae; 18 Subsp. kenyae; 19 Sacillales; Bacillaceae; Bascillus thuringlensis. 1 J.Y., Shim H.J., Boo K.S.; 1 the EMEL/GenBank/DDBJ dat; 19.1;
MIN BBLr BBLr C pp Pp Pp Pp Pp Pp Pp Pp Pp Pp Pp Pp Pp P	
RESULT 1 QG FYWG AC GFYWG AC GFYWG DT 05-JUL-2004 (TERMBLE) B CTyl type crystal prote B acillus thuringlensis C CYL type crystal prote B Acillus TaxID=33930; NOSI TaxID=33930; NOSI TaxID=33930; NOSI TaxID=33930; RA SEQUENCE FROM N.A. RA SEQUENCE FROM N.A. RA SIDMITTER (MAR-2004) TERM SIDMITTER (MAR-2004) TERMS SIDMITTER (MAR-2004) TERMS SIDMITTER (MAR-2004) TERMS SIDMITTER SIDMIT	Query Match Best Local Similarity Matches 8; Consex
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RESULT 3 CLJA_BACTU

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
50-MAY-2004 (Rel. 44, Last sequence update)
65-UJL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylub (Insecticidal delta-endotoxin
Cryll(b) (Crystaline entomocidal protoxin) (134 kDa crystal protein).
Name=crylub; Synonyms=crylu(b), cryErl;
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=T7123.9;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                   lepidopteran insects.";
Patent number US5356623, 18-OCT-1994.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae. Toxic to Plutella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the spore coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                          sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Federspiel N.A., Conway A.B., Conway A.R., Davis K., Brendel V.,
                                                                                                                                                                                                                                                                                                                                                                                                     xylostella.
DEVELOPMENTAL STAGE: The crystal protein is produced during
                                                                                                                                                                                                                               SEQUENCE FROM N.A. STANDALL BLANDAL, STRANDENEL B-18973 / EG5092; STRANDEL B-18973 / BOAZALEZ J.M. Jr.; WON TERSCH M.A., Gonzalez J.M. Jr.; Bacillus thuringiensis cryET1 toxin gene and protein toxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sporulation; Toxin.
SEQUENCE 1170 AA; 133553 MW; B053B9619B78DC19 CRC64;
                                                                                                                                                          Bacteria; Firmičutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-07AN-1998 (TrEMBLrel. 05, Created)
01-07AN-1998 (TrEMBLrel. 05, Last sequ
01-0CT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfan; PP03944; Endotoxin_C; 1.
Pfam; PP00555; Endotoxin_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03945; Endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U31527; AAA98959.1; -.
HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S LLRYLADNFLPGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::| :||:||
LLOFLLNNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CER1-like protein.
                                                                                                                                                                                    NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIR=NRRL B-21110 / EG5847;
STRAIR=NRRL B-21110 / JGD C.S., Gondalez J.M. Jr.;
Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to lepidopteran insects."
Patent number US5322667, 21-UWN.19
- I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae.
- I- DEVELOPMENTAL STAGE: The cryetal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylar (Insecticidal delta-endotoxin.
CrylJ(a)) (Crystaline entomocidal protoxin) (133 kDa crystal protein).
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                           Score 48; DB 2; Length 782;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporulation; Toxin.
SEOUENCE 1167 AA; 132760 MW; 3B7357D14E655FC7 CRC64;
                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-crylda, Synonyms-cryld(a), cryET4;
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the delta endotoxin family.
                    89009 MW; 36990BD477860DB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Pred. No. 59;
4; Mismatches
                                                                                                                                                                                                                                                                                                   PRT; 1167 AA.
                                                                               Pred. No. 39;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001176; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_N:
Pfam; PF03945; Endotoxin_M: I.
Pfam; PF03945; Endotoxin_N: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L32019; AAA22341.1; -. HSSP; P02965; 1CIY.
                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                 5 LLRYLADNFLPGG 17
                                                                                                                                                                                          35 LLQFLLNNFVPGG 47
                                                                                                                                                                                                                                                                                                     STANDARD;
  782 7
782 AA;
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CLUB_BACTU
ID _CLUB_BACTU
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Q45738;
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PRT; 1170 AA.

STANDARD;

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NCBI_TaxID=3702;
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N [1]

N [2]

Deng M.D., Peng S., Lemieux B.;

A "Genomic (Accession No. X95964) and cDNA (Accession No. X95965)

RT "Genomic (Accession No. 185964) and cDNA (Accession No. X95965)

RT sequences of the CER1-like gene of Arabidopsis thaliana derived from a plant DNA/T-DNA insertion junction. (PGR96-019).";

RL Plant Physiol. 110:1436-1436 (1996).

DR GO; GO:0008124; F:catalytic activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR006089; Sterol_desat.

InterPro; IPR006089; Sterol_desat.

"f-m. PP01598; Sterol_desat."

"f-m. PP01598; Sterol_desat."
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Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Buehler B., Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O., Osborne B., Shen Y., Toriumi M., Vyotskaia V., Yu G., Theologis A., Ecker J., Davis R.W.,
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, 189959; AACA4373.1. -
GO; GO:0008152; F:catalytic activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR006087; Sterol desat.
InterPro; IPR006088; Sterol desat.
Ffam; PF01598; Sterol desat.
SEQUENCE 604 AA; 69334 MW; BOC46279AA473782 CRC64;
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantue; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Suranatophyta; Massicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                  Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 622;
                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                 DB 2;
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Pred. No. 46;
                                                                                                                                                                                                                                                                            622 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 AA
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                 Score 47;
Pred. No.
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                      3;
                                                                                                                                                                                                                  100 IFNTLLMYLANIKLPGAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 IFNTLLMYLANIKLPGAS 117
                                                                                                                                                                                               1 LFSVLLRYLADNFLPGGS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                  51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.6%;
                                                                                                                                                                                                                                                                                   039046,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT_2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LFSVLLRYLADNFLPGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.6
....hes 10; Conservative
                                                                                                                                                 Query Match 51.6
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CER1-like protein.
Name=CER1-like;
                                                                                                                                                                                                                                                                                                                                  CER1-like protein.
Name=CER1-like;
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             039047;
                                                                                                                                                                                                                                                                           Q39046
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                                                                                                                                                                                                                                                      9
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Q39047
                                                                                                                                                                                                                                                    SCREARE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Deng W.D., Peng S., Lemieux B.;

Deng W.D., Peng S., Lemieux B.;

Deng W.D., Peng S., Lemieux B.;

"Genomic (Accession No. X95965)

sequences of the CER1-like gene of Arabidopsis thaliana derived from a plant bNA insertion junction. (PGR96-019).";

EMBL, X95965; CAA65200.1;

EMBL, X95965; CAA6520.1;

EMBL, X95965; CAA65200.1;

EMBL, X95965; CA
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MEDLINE=20153186; PubMed=10688690;

MEDLINE=20153186; PubMed=10688690;

"Cloning of two new cry genes from Bacillus thuringiensis subsp.

"Cloning of two new cry genes from Bacillus thuringiensis subsp.

"Cloning of two new cry genes from Bacillus thuringiensis subsp.

"Cloning of two new cry genes from Bacillus thuringiensis subsp.

"Cloning of two new cry genes from Bacillus thuring to the midgut epithelial cells of legidopteran larvae. Toxic to Pieris rapee.

-!- DEVELOPMENTAL STAGES: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylGb (Insecticidial delta-endotoxin CrylG(b)) (Grystaline entomocidal protoxin) (133 kDa crystal protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2; Length 623;
Pred. No. 46;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=cryIGb; Synonyms=cryIG(b), cryH2, Bacillus thuringiensis (subsp. wuhaensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=52024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001178; Endocoxin.
Interpro; IPR005639; endocoxin.
Interpro; IPR008639; endocoxin.
Interpro; IPR008979; Gal_bind_like.
Pfam; PP03944; Endocoxin_C; 1.
Pfam; PP03945; Endotoxin_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 IFNTLLMYLANIKLPGAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LFSVLLRYLADNFLPGGS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.6%;
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces sp. AM-7161.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=221710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.5%; Score 46; DB 2; Length 282; larity 64.3%; Pred. No. 30; Conservative 2; Mismatches 3; Indels
Query Match 50.5%; Score 46; DB 2; Length 280; Best Local Similarity 60.0%; Pred. No. 30; Matches 9; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Transmembrane; Transport.
SEQUENCE 282 AA; 30199 MW; 1AFE04BB6512BDF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                               282 AA.
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                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter permease protein.
OrderedLocusNames=blr3339;
                                                                                                                                                               211 VFRVLLRYLSDREVP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||:||:| | ||
185 FSVVLRFLLPNILP 198
                                                                                                                          1 LFSVLLRYLADNFLP 15
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                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Name=med-ORF18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=375;
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01-JUN-2003
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                                                                                                                                                                                                                                                                       RESULT 11
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Embli, AF237388; AAF73951.1; -. SEQUENCE .280 AA; 31498 MW; 230869401568DDA6 CRC64;
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                                                                                                                                Gapa
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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Pred. No. 87;
3; Mismatches 3; Indels
                                                                Score 47; DB 1; Length 1169; Pred. No. 87;
            1169 AA; 132904 MW; DIEFCI508A8B10BD CRC64;
                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li C., Zhang J., Li G., Huang D.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288683; AAO13756.1; -.
HSSP; P02265; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 0005102; F: receptor binding; IEA. GO; GO: 0006952; P: defense response; IEA. GO; GO: 0006405; P: pathogenesis; IEA. INTERPRO; IPR001178; Endotoxin.

InterPro; IPR005638; endotoxin.C.

InterPro; IPR005639; endotoxin.N.

InterPro; IPR008539; endotoxin.N.

Pfan; PF00344; Endotoxin.C.; I.

Pfam; PF00555; Endotoxin.C.; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                   Similarity 57.1%;
8; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                        5 LLRYLADNFLPGGS 18
                                                                                                                                                                                                                         S LLRYLADNFLPGGS 18
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                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03945; Endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta-endotoxin Cryl
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=B-Pr-88;
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Name=ampE;
                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     Q8GHE8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KIB5
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                                                                                                                                                                                                                                                                                                                                                                                               Q8GHE8
                                                                                                                                   Matches
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Q8GHE8
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Gaps

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184 VILPYLARGFLDGGS 198

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CRAIN=CLIP 11262 / Serovar 6a;

STRAIN=CLIP 11262 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669;

Allaser P., Frangeul L., Buchrisser C., Rusnick C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chercuani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chercuani F., Couve B., de Daruvar A., Dehoux P.,

Batian K.-D., Faihi H., Garcia-del Portillo F., Durant L., Dussurget O.,

Butiar L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Mattcurnan A., Matta Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Comparative genomics of Listeria species.";

Comparative genomics of Listeria species.";

EMBL; AL596165; CAC95724.1; -..

REMBL; AL596165; CAC95724.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R HISSP; PAT1278; AUG494.

R HISSP; PAT1278; AUG494.

R G0; G0:000518; P:electron transport; IEA.

G0; G0:000518; P:electron transport; IEA.

R G0; G0:000518; P:electron transport; IEA.

R G0; G0:000518; P:electron transport; IEA.

R InterPro; IPR00132; PAD_DY_redox.

R InterPro; IPR00135; PAD_DY_redox.

R InterPro; IPR001155; Oxidored FMN.

R InterPro; IPR001155; Oxidored FMN.

R Pfam; PF00724; Oxidored FMN.

R PRINTS; PR00419; PADRAPASE.

R PRINTS; PR00469; PADRAPASE.

R PRODOM; PD000139; FAD. R.

R ProDom; PD000139; FAD. R.

COMDITED FAD. R.

COMDITED FAD. R.

R ProDom; PD000139; FAD. PYT redox; 1.

COMDITED FAD. R.

SEQUENCE 664 AA; 72912 MW; 57CA1857181B205D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 664;
                                                                                                                                                                                                                                                                                               Listeria innocua.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lmo0489 protein.
OrderedLocusNames=lmo0489;
Listeria monovytogenes.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.5%; Score 46; DB 2; 47.1%; Pred. No. 72;
                                                                                                                                    664 AA
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FPIVLRFSADEFTEGGN 234
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                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                           OrderedLocusNames=lin0492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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les 8; Conserv
                                                                                                                                                                                                                                                          Lin0492 protein.
                                                                                                                                                                               01-DEC-2001
01-DEC-2001
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Q8Y9N6 ;
                                                                                                                                                           Q92EG8;
                                                                                       RESULT 14
092EG8
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RC STRAIN=AM-7161,

RX MEDLINE=2273958; PubMed=12855716;

RT Ichinose K., Ozawa M., Irou K., Kunieda K., Ebizuka Y.;

RI Cloning, sequencing and theterologous expression of the medermycin accomparative analysis of the benzolsochromanequione gene clusters.";

RI comparative analysis of the benzolsochromanequione gene clusters.";

Ricrobiology 149:1633-1645(2003).

-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.

-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.

-!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase a. . .; IEA.

EMBL, AB103463; BA750291.;

EMBL, AB103463; BA750291.;

EMBL, AB103463; BA750291.;

EMBL, AB103463; BA750291.;

EMBL, AB103463; NTP-transferase.

InterPro; IPRO05908 GJE-thy trans.

InterPro; IPRO05835; NTP-transferase.

ITGRRAMS; TIGRO108; rmlA long; 1.

TIGRRAMS; TIGRO108; rmlA long; 1.

KM Kinase; Nucleotidyltransferase;

KW Kinase; Nucleotidyltransferase;

SEQUENCE 354 AA; 37083 MW; 8002BCF931ABAB51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22828889; PubMed=14500908;

MEDLINE-22828889; PubMed=14500908;

Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,

Nandakunar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Myer F., Lederer H., Schuster S.C.;

"Complete genome sequence and analysis of Wolinella succinogenes.";

Froc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).

EMBL; BX571662; CAEILI83.1;

RO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). .; IEA.

RO; GO:0004665; P:asparagine blosynthesis; IEA.

RO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001962; Asn. Synthase.

InterPro; IPR006456; Asn. Synthase.

InterPro; IPR006483; GATase_2:

Rem; PF00733; Asn. Synthase.

Pfam; PF007310; GATase_2: 1.
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteracea, Wolinella.
NCBI_TaxID=844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ (BC 6.3.5.4).
Name-PAB1605; OrderedLocusNames=WS2192;
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome, Ligase. SEQUENCE 606 AA, 71101 MW, 4C01CD1B7F4DDD16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.5%; Score 46; DB 2; Best Local Similarity 66.7%; Pred. No. 66; Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR01536; asn_synth_AEB; 1.
PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 YLGDNMLPGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 YLADNFLPGG 17
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STRAIN=DSMZ
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Query Match

Best Loc Matches

Q7MBG3 Q7MBG3;

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RESULT 13 Q7MBG3

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Gaps

NCBI_TaxID=1639;

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0
                                                           REDUINE_21537279; PubMed=11679669; Rusniok C., Amend A., Glaser P., Frangeul L., Buchrieter, Brandt P., Chakraborty T., Glaser P., Frangeul L., Buchrieter, Brandt P., Chakraborty T., Glaser P., Reangeul L., Buchrieter, Duchade B., Durant L., Dussurget O., Entian K.-D., Falli H., Gamez-Gel Portillo P., Garrido P., Garrido P., Shift H., Garrido P., Haif T., Hauf J., Jackson D., Gautter L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Andere L. M., Kaeret U., Kraft J., Kunh M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Norellas S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schluter T., Sinces N., Tierre A., Purcell R., Andrews G., Schluter T., Sinces M., Tierre A., Purcell R., Andrews G., Schluter T., Sinces M., Tierre A., Purcell R., Andrews G., Maita Vicente J., Ng E., Nedjari H., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P., Remmel B., Rose M., Schluter T., Sinces M., Tierre P., Purcell R., Schluter T., Sinces M., Paras J., Paras J., Paras J., Paras J., Janes M., Schluter T., Sinces M., Janes J., Mallis J., Janes J
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                                                     SEQUENCE FROM N.A.
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Search completed: November 10, 2004, 14:50:06 Job time: 25.9774 secs

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Scoring table:

Searched:

Perfect score:

Seguence:

OM protein

Run on:

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Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 31076, A
Sequence 70, Appl
Sequence 7660, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 119, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6534, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENEET.054PR.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6534
US-09-620-412C-245

US-09-598-410-245

US-09-489-039A-13022

US-08-464-117-24

US-08-463-117-24

US-08-463-177-24

US-09-491-577-70

US-09-491-577-70

US-09-491-577-70

US-09-491-577-70

US-09-710-279-3196

US-09-710-279-3196

US-09-318-328-325-6191

US-09-328-325-6191

US-09-318-325-6191

US-09-318-325-6191

US-09-318-325-6191

US-09-134-001C-4629
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Sequence 6991, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Profitte OF INVENTION: ESTS and Encoded Human Profitte OF INVENTION: ESTS and Encoded Human Profitte OF INVENTION DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6991
LENGTH: 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.8
Warches 10; Conservative
   TYPE: PRT
CRGANISM: Homo sapiens
US-09-621-976-6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-6991
     RESULT 1
US-09-621-976-6534
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US-09-621-976-6991
   Query Match
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                                                                                                                       November 10, 2004, 13:44:14; Search time 6.58868 Seconds (without alignments)
181.178 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-6991
US-09-54-6812-7788
US-08-464-517-6
US-08-464-517-6
US-08-464-517-23
US-08-464-517-23
US-08-464-517-23
US-08-463-772-23
US-08-26-877-246
US-09-556-877-246
US-09-556-877-247
US-09-556-877-247
US-09-556-877-247
US-09-556-877-247
US-09-556-877-247
US-09-598-419-247
US-09-598-419-247
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US-09-598-419-247
US-09-598-4528-596
US-09-511-9990-7713
US-08-26-3618-50
US-08-26-3618-50
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US-08-26-571-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                       sw model
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102
1 DWQVLLGKLLWKIDNPGI 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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      4444444444444444

      666664

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Score

Result Š. 42.5

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44.6%; Score 45.5; DB 2; Length 280;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

44.6%; Score 45.5; DB 3; Length 280;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08463772
Sequence 6. Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/483,772

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-07-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-WAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REPERSUE/DECKET NUMBER: 36,709
REPERSUE/DECKET NUMBER: 36,709
REPERSUE/DECKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTEX: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (LEXE)
CURSTEAT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5940
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                             127 DWEVLVLGKLKWDL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                       LENGTH: 280 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 1 DWQVL-LGKLLWKI 13
                                                                                                                                                           MOLECULE TYPE: protein US-08-464-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-463-772-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-463-772-6
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                                                                                                                                                                                                                                                                                       APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 2000-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7788
LENGTH: 189
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                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-464-517-6
is Sequence 6, Application US/08464517
is Patent No. 5869640
is GENERAL INFORMATION:
APPLICANT: BEACH, David H.
ITILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
CITY: Boston
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                                 5; Indels
       Best Local Similarity 58.8%; Pred. No. 2.3; Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION NUMBER: US/08/464,517
FILING DATE:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/889,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/889,178
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAWAY: WALCHAMATION:
NAWAY: WALCHAMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
                                                                                                                                                                                                                                          Sequence 7788, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DW-----QVLLGKLLWKIDNPG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 DWFHMIPAVLLGSLLPDLDHPG 52
                                                                            2 WOVLLGKLLWKID-NPG 17
                                                                                                          20 WSQLLRRLRWKDDLNPG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: Proteus mirabilis
US-09-543-681A-7788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                          US-09-543-681A-7788
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US-246.361A-6

JOS-246.361A-6

JOS-246.361A-6

JOSTORRAL INTORNATION:

TITLE OF INVENTION:

APPLICANT:

BEACH, David H.

TITLE OF INVENTION:

JOSTORES RELATED THERETO

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY:

COMPITE: MA

COMPITE: MA

COMPITE: EN PROPONISH

COMPITE: IS PROPONISH

FILING DATE: 19-001-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-001-1992

PRIOR APPLICATION PATA:

APPLICATION NUMBER: US 07/963,178

FILING DATE: 16-001-1992

PRIOR APPLICATION NUMBER: US 07/963,178

FILING DATE: 16-001-1992

PRIOR APPLICATION NUMBER: US 07/963,178

FILING DATE: 16-001-1992

PRIOR APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

PRIOR APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

PRIOR APPLICATION PATA:

APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

PRIOR APPLICATION PATA:

APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

PRIOR APPLICATION PATA:

APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

PRIOR APPLICATION PATA:

APPLICATION NUMBER: US 07/101,514

FILING DATE: 16-001-1992

ATTOMICATION PATA:

APPLICATION NUMBER: US 07/101,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

44.6%; Score 45.5; DB 2;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2;
              PAPELICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIPTCATION: 435
CLASSIPTCATION: 435
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-07-1992
APPLICATION NUMBER: US 07/88,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATE: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-490
TELEPHONE: (617) 227-400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDENESS: single
TOPPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|| |||| :
139 DWEVLVLGKLKWDL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DWQVL-LGKLLWKI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-464-517-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-246-361A-6
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Sequence 23, Application US/08464517

GENERAL INFORMATION:

APPLICANT: BEACH, David H.

ITILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50

CORRESPONDENCES: 50

STREE: ADDRESSEE: LAHIVE & COCKFIELD

STREE: ADDRESSEE: LAHIVE & COCKFIELD

STREE: MA

COUNTY: USA

ITILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

CORRESPECT: 60 State Street

CITY: BOSCON

STRIE: MA

COMPUTER: DA

COMPUTER: THE PORPY disk

COMPUTER: THE PROCOMPATION: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)
                                                                                                             Sequence 6, Application PC/TUS9305000
Sequence 6, Application PC/TUS9305000
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5; DB 5; Length 291;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALPY 021/3

CARPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: Date Ploppy disk
COMBUTER: Patent In Pelease #1.0, Version #1.25
CORREATION SYSTEM: PCT/US93/05000
GURSENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION DATA:
PRICASIFICATION DATA:
PRICASIFICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,22
REPERBORG/POCKET NUMBER: CSHL91-02A
TELEPHONE: 617-661-9540
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: AMINO ACID
TYPE: MAINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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127 DWEVLVLGKLKWDL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 DWEVLVLGKLKWDL 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DWQVL-LGKLLWKI 13
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Best Local Similarity 64.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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                                                                                                             PCT-US93-05000-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-05000-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-464-517-23
                                                                               RESULT 6
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Sequence 23, Application US/08463772

Sequence 24, Application US/08463772

Setent No. 6066501

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD
STREET: 60 State Street
CITY: Boston
CITY: MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.6%; Score 45.5; I
ilarity 64.3%; Pred. No. 20;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 10435
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
PILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE DOCKET NUMBER: MII-004C
TRLECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCIII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
                                            ||:|| |||| |:
|139 DWEVLVLGKLKWDL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 DWEVLVĽĠKĽKWDL 152
                      1 DWQVL-LGKLLWKI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DWQVL-LGKLLWKI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                USA
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PCT-US93-05000-23
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                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
44.6%; Score 45.5; DB 2; Length 292;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.5; DB 2; Length 292;
Pred. No. 20;
2; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHWARE ASCIII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/881,178
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER: MII
TELECOMONICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                          139 DWEVLVLGKLKWDL 152
                                                                                                                         i ENGTH: 292 amino acids
i TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-246-361A-6
                                                                                                                                                                                                                                                                                                                                      1 DWQVL-LGKLLWKI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // MOLECULE TYPE: peptide US-08-246-361A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Gaps

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Gaps
                           Sequence 247, Application US/09556877
; Sequence 247, Application US/09556877
; Patent No. 6423916
; Patent No. 6423916
; Patent No. 6423916
; APPLICANT: Batia, Ajay
APPLICANT: Skeiky, Yasir
; APPLICANT: Ring, Steve
APPLICANT: Ring, Steve
; TTLLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: COMPOSITIONS
; TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION UNDERS. US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; SEQ ID NO 247
; SEQ ID NO 247
; LEMGTH: 20
; WUDD: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 246, Application US/09620412C

Patent No. 644824

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERBRICE: 210121.46607

CURRENT PILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: PastSEQ for Windows Version 3.0/4.0

SEQ ID NO 246

LENGTH: 20
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Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven F. Fling
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 4; Length 20; Pred. No. 1.4;
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Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Made in a lab
US-09-620-412C-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Made in a lab
US-09-556-877-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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US-09-620-412C-246
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US-09-620-412C-247
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Sequence 246, Application US/09556877

Security Probat.

APPLICANT: Bhatia, Ajay

APPLICANT: Skeiky, Yasir

APPLICANT: Shaiky, Yasir

APPLICANT: Fling, Steve

APPLICANT: Fling, Steve

APPLICANT: Fling, Steve

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DAMBGROSIS OF CHLAWYDIAL INFECTION

FILE REFERENCE: 210121.469C5

CURRENT APPLICANTON: DATE: 2000-00-19

NUMBER OF SEQ ID NOS: 305

SOFUTANTE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 246

LENGTH: 20
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Pred. No. 1.4;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                 COMPUTE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERRACE/DOCKET NUMBER: CSH191-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHRACTERISTICS:
1 PROTEIN OF THE SECOND NO: 23:
SEQUENCE CHRACTERISTICS: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Made in a lab
US-09-556-877-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Lexington
Massachusetts
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US-09-556-877-246
                   STATE: M
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Search completed: November 10, 2004, 14:55:36 Job time: 6.63868 secs

Sequence 162659, Sequence 133339, Sequence 200791, Sequence 200791, Sequence 200791, Sequence 275, App Sequence 246, App Sequence 247, App Sequence 24, App Sequence 12, App Sequence 12, App Sequence 396, App Sequence 57798, Aspenence 22672, Sequence 286181, Sequence 28672, Aspenence 28672, Aspenence 2877, App Sequence 28787, App Sequence 287887, App Sequence 28787, App Sequence 28787,

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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Sequence 49, Application US/10092750

publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Almin, Julia
APPLICANT: Almin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENITON: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PRISESE for Windows Version 4.0
SEQ ID NO 49

LEMOTH: 18
6 US-10-427-963-162659

5 US-10-424-599-216482

6 US-10-437-963-200793

6 US-10-437-963-200793

6 US-10-437-963-200793

4 US-10-16-275-276

4 US-10-408-765A-88

US-09-841-132-246

US-09-841-132-246

US-10-767-71-32655

US-10-767-71-315440

5 US-10-425-114-41567

6 US-10-369-435-24

105-09-841-132-441

5 US-10-369-435-39

105-09-841-132-441

105-09-841-132-441

105-09-841-132-441

105-09-841-132-441

105-09-841-132-441

105-09-841-132-441

105-09-841-132-398

105-10-369-435-36

105-10-369-435-36

105-10-425-114-65642

105-10-425-114-65642

105-10-425-114-65642

105-10-425-114-65642

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105-10-425-115-266181

105-10-425-115-266181
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US-10-424-599-210109
US-10-437-963-152062
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100.0%; Score 102; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-10-424-599-216294
; Sequence 216294, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-10-092-750-49
    RESULT 1
US-10-092-750-49
    셤
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Sequence 216294,
Sequence 222731,
Sequence 56899, A
Sequence 125535,
Sequence 125535,
Sequence 12522,
Sequence 195522,
Sequence 130091,
Sequence 169611,
Sequence 169611,
                                                                                                                                         November 11, 2004, 01:28:30; Search time 20.8189 Seconds (without alignments) 305.399 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/PCT_TEW_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_TEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/PCT_TEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO_FUBGOMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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5 US-10-425-1529-216294

7 US-10-425-115-289398

6 US-10-425-115-289398

6 US-10-425-115-289398

6 US-10-437-963-125535

6 US-10-437-963-13552

6 US-10-437-963-13952

6 US-10-437-963-13952

8 US-10-445-599-276306

5 US-10-445-599-276306

6 US-10-445-599-276306

5 US-10-437-963-13338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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102
1 DWQVLLGKLLWKIDNPGI 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length DB
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144
6444
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Gaps

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Indels

12110987654321

Length 18;

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Sequence 125535, Application US/10437963
; Sequence 125535, Application US/10437963
; Publication No. US2040123343A1
; CGNERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Zhou, Yihua
    APPLICANT: Zhou, Yihua
    APPLICANT: Applicant Construction of the Molecules Applicant: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Brad
    APPLICANT: Boukharov, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(53221)B
    CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125535
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 289398, Application US/10425115
; Bublication No. US20040214272A1
; GENERAL INFORMATION; US20040214272A1
; GENERAL INFORMATION; Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REPRENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; KURRENT FILING DATE: 2003-04-28
; KURDEN OF SEQ ID NOS: 369326
; SEQ ID NO 289398
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                                                                                                                                                                                                                 Length 144;
                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_27020C.1.pep
US-10-425-115-289398
                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0%; Pred. No. 16;
Matches 8; Conservative 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(649)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: 30950545.pep
US-10-767-701-56899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DWQVLLGKLLWKIDNP 16
                                                                                                                                                                                                                                                                                                                  1 DWOVLLGKLLWKIDNP 16
                                                                                                                                                                                                                                                                                                                                               | ::|: |:| ||| ||| 84 DKKILVDMLIWAIDNP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 DKKILVDMLIWAIDNP 99
                                     LENGTH: 144
TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
             SEQ ID NO 56899
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: APLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 292731, Application US/10425115
Sequence 292731, Application US/10425115
Sequence 292731, Application US/104272A1
Sequence 292731, Application US/104272A1
SEQUENCE CANAIN CASCA, Thomas J.
APPLICANT: Excelle, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REPRENCES 382-1 (53222) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 292731
LENGTH: 116
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Sequence 56899, Application US/2084A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cor INVENTION:
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: PAT_MRT3847_37342C.1.pep
US-10-424-599-216294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_30053C.1.pep
US-10-425-115-292731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%; Score 52; DB 15; ilarity 50.0%; Pred. No. 6.3; Conservative 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
48.0%; Score 49; DB 17;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 DMKILVDMLLWAVDNP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DWQVLLGKLLWKIDNP 16
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                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
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US-10-425-115-292731
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US-10-767-701-56899
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Sequence 130091, Application US/10437963

Sequence 130091, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION

BAPLICANT: La Rosa, Thomas J.

APPLICANT: Shou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Buckharov, Andrey A.

APPLICANT: Buckharov, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                      ..
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                                                                                                                                                Length 446;
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                                                                                                                                                                                                   1; Indels
LOCATION: (1)...(446)
CTHER INFORMATION: unsure at all Xaa locations
FRATURE:
CTHER INFORMATION: Clone ID: PAT_MRT4530_91462C.1.pep
US-10-437-963-195522
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64.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 4;
                                                                                                                                                   ; DB 16;
. 1e+02;
                                                                                                                                                Score 47; DB 1
Pred. No. 1e+02
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT PEDIGATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
SOFTWARE: PARENT NOWER: 300
SOFTWARE: PARENT NET: 300
SOFTWARE: PARENT NET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6653, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                      Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VLLGKLLWKIDNPG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VLLGSLLWPLAAPG 28
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285 LLGKRLWKLEN 295
                                                                                                                                                                                                                                                      5 LLGKLLWKIDN 15
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OZAKI, AKIO
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Matches 9; Conserv
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Sequence 19552. Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Fing

ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 195522

LENGTH: 4446
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 310459, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION
UNMER: 38-21 [5322] B
CURRENT FILING DATE: 2003-04-28
FOURTH FILING DATE: 2003-04-28
FOURTH FILING DATE: 2003-04-28
FOURTH FILING DATE: 2003-04-28
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                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2816C.1.pep
US-10-437-963-125535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47.5; DB 17;
Pred. No. 90;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_46196C.1.pep
US-10-425-115-310459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DWQVLLGKLLW------KIDNPG 17
                                                                                                                                                                                                                                                                                    2 WQVLLGKLLWKIDNPG 17
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Best Local Similarity 30.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                 2 WKQLLGKISWKAPKSG 17
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ORGANISM: Oryza sativa
                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 477
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Sequence 133338

Sequence 133338

Sequence 133338

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Resa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 13338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 162659, Application US/10437963
; Sequence 162659, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GRNERAL INPORVATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162659
; LENGTH: 305
; TYPE: PRT
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Pred. No. 67;
4; Mismatches 2; Indels
                                                                                                                                            Length 156;
; TYPE: PRT
; ORGANISM: Glycine max
; PEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_124172C.1.pep
US-10-424-599-169611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_35218C.1.pep
US-10-437-963-133338
                                                                                                                                          Score 46; DB 15;
Pred. No. 49;
                                                                                                                                                                                            4; Mismatches
                                                                                                                                     45.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                           7 GKLLWKIDNPG 17
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Avail David X
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SEFERNCE: 38-21(5323)
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 276306
LENGTH: 152
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Sequence 169611, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 156
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45.1%; Score 46; DB 15; Length 152;
Best Local Similarity 43.8%; Pred. No. 47;
Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_32286C.1.pep
US-10-437-963-130091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: PAT_MRT3847_91523C.1.pep
US-10-424-599-276306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(152)
OTHER INFORMATION: unsure at all Xaa locations
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 130091
LENGTH: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 DKKILVDMLFWAVDNP 109
                                                                                                                                                                                                                                                                                                                                                               1 DWQVLLGKLLWKIDNP 16
                                                                                                                                                                                                                                                                                                                                                                                          84 DKKILVDMLFWAIDNP 99
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                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-276306
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                                                                                                                                                                          FEATURE:
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RESULT 15

US-10-424-599-218482

US-10-424-599-218482

Sequence 218482, Application US/10424599

SUBJICATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Avoil David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 218482

LENGTH: 312.
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Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                            Score 46; DB 16; Length 305;
Pred. No. 96;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_39317C.1.pep
US-10-424-599-218482
ORGANISM: Oryza sativa
FATURE:
CTHER INFORMATION: Clone ID: PAT_MRT4530_6172C.1.pep
US-10-437-963-162659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRI
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .. (312)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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260 KALLGKWIWKLEN 272
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: Movember 10, 2004, 13:40:53 ; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec

Title: US-10-092-750-49
Perfect score: 102
Sequence: 1 DWQVLLGKLLWKIDNPGI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

laximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:*

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			hypothetical prote		hypothetical prote	probable transcrip	transcription regu	phytoene synthase-	m	allantoicase (EC 3	60K cysteine-rich	60K cysteine-rich	60K cysteine-rich		60K cysteine-rich	60 kDa Cysteine-ri	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable lysyl-tRN	membrane protein y	hypothetical prote	ă	cell cycle protein	probable transfera	~	м	hypothetical prote	hypothetical prote	
	£	TD	T33259	G86815	T29556	F97387	AG2605	\leftarrow	N	A35829	$^{\circ}$	B43584	D71515	C81671	S12602	A86560	T48012	C85823	E90976	C70627	T36123	B64963	T31014	AB2373	D64743	D81868	4801	05	T39047	52	8380
	0																												7		
	1000	rengru	309	207	254	258	290	275	292	354	547	547	553	554	556	556	613	107	107	210	545	547	1025	135	432	276	279	355	778	968	300
*	Query	March	50.0	49.0	47.1	47.1	47.1	45.1	44.6	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	43.1	43.1	43.1	43.1	43.1	43.1	42.6	42.6	42.2			42.2		41.2
		SCOLE	51	20	48		48	46	45.5	45	45		45		45			44	44			44	44	43.5	43.5	43	43	43	43	42.5	42
	Result	0 1	н	7	e	4	2	9	7	ω	6	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

49.0%; Score 50; DB 2; Length 207; 61.1%; Pred. No. 2;

Query Match Best Local Similarity

formate dehydrogen	hypothetical prote	probable minor str	acetohydroxy acid	acetolactate synth	fimbrin-like 71 X	beta transducin -	hypothetical prote	two-component hybr	hypothetical prote	cyclin-like protei	cyclin D3 - rat	hypothetical prote		hypothetical prote	hypothetical prote
\$18215	G75011	T13635	G86062	F91216	JC7170	T40510	A86222	AC2236	A84647	C40035	JC4012	AB1475	T24972	T24970	S75753
-	N	(1	~	0	N	~	~	7	7	N	7	~	N	N	7
306	402	512	548	548	579	736	810	865	1660	237	293	553	639	698	240
41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	40.7	40.7	40.7	40.7	40.7	40.2
42	42	42	42	42	42	42	42	42	42	41.5	41.5	41.5	41.5	41.5	41
30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 T33259
	Dairis elegans
	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C:Accession: T33259
	R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D. sihmitted to the RMR. Data Library. May 1998
	A; Description: The sequence of C. elegans cosmid C24B9. A; Reference number: Z21310
	A;Accession: T33259 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Anolecule type: DNA A;Anolecule type: And
	Ajrasaludes: 1-20 km/R. Ajrasa-references: UNIPROT:076432; EMBL:AF068709; PIDN:AAC19253.1; GSPDB:GN00023; CES! AjExperimental source: strain Bristol N2; clone C24B9
*	C;Genetics: A;Gene: CESP:C24B9.2 A;Map position: 5 226/1; 273/1; 298/3 A;Introns: 187/3; 226/1; 273/1; 298/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C16D9.7
	Query Match 50.0%; Score 51; DB 2; Length 309; Best Local Similarity 40.0%; Pred. No. 2.2; Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
	Oy 1 DWOYLLGKLIWKIDN 15 :: :: Db 258 BWMIVLAQLLWQLDH 272
	RESULT 2 G86815 NADH dehydrogenase yphA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Species: 23Mar-2001 #sequence_revision 23Mar-2001 #text_change 09-Jul-2004 C;Accession: G86815 R;Bolotin, A.; Wincker; P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Rolecule type: DNA A;Residues: 1-207 <sto> A;Residues: 1-207 <sto> A;Residues: Teferences: UNIPROT:09CFF1; GB:AE005176; PID:g12724526; PIDN:AAK05625.1; GSPDB A;Residuental source: strain IL1403 C;Genetics: A;Gene: yphA</sto></sto>

Matches

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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-275 <TET>
A;Cross-references: UNIPROT:Q9UYLB; GB:AE002501; GB:AE002098; NID:g7226755; PIDN:AAF418
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NiAlternate names: PRADI/cyclin D1 proto-oncogene homolog C;Species: Homo sapiens (man) E44022; A44022; E60850 C;Accession: B42822; A44022; E60850 D; Ward, D.C. Genomics 13, 575-584, 1992 A;Title: Molecular cloning and chromosomal mapping of CCND genes encoding human D-type A;Reference number: A42822; MUID:92347881; PMID:1386336
                                                                                                                                                                                                                                                                                                                                     A;cross-references: UNIPROT:08UIQ4; GB:AE008688; PIDN:AAL41261.1; PID:g17738567; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rifettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Socience 287, 1809-1815, 2000
A,Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; A;Retence number: Agloome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Accession: H81074
A;Status: preliminary
A;Mocession: H81074
A;Status: preliminary
A;Mocession: A;Mocession: Mulp. 20175755; PMID: 10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phytoene synthase-related protein NMB1521 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81074
                                                                                                                                                                                 C58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 290,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 2;
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: Atu0239
A;Map position: circular chromosome
C;Accession: AG2605
R:Wood, D.W.; Setubal, J.C.; Kaul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 DWÓSRĽSDĽĽWKHSN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%;
ilarity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%;
58.3%;
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DWLIMLKKALWK 275
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-290 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-292 <XIO>
                                                                                                                                                                                                                                                           Status: preliminary
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                                                                                                                                                                                                                                probable transcription regulator (PA2489) [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens (c;Species: Bo-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 ***
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefacient monder: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: F97387
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: UNIPROT:Q8UIQ4; GB:AE007869; PIDN:AAK86055.1; FID:g15155128; GSPDB:G
C;Genetics:
A;Gene: AGR C 407
A;Map position: circular chromosome
C;Superfamily: arabinose operon regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [imported] - Agrobacterium tumefaciens (str
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C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
          Gaps
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47.1%; Score 48; DB 2; Length 254;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 6; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.1%; Score 48; DB 2; Length 258; 60.0%; Pred. No. 5.3; tive 0; Mismatches 6; Indels
          Indels
          7;
          Mismatches
          ö
                                                                                                  DWOELLOKSDWVIDAVGI 74
                                                         1 DWQVLLGKLLWKIDNPGI 18
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198 EWIIVLAQLLWQLDH 212
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          11; Conservative
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ઠ q Query Match Best Local S Matches 9

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RESULT 5

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R;Allen, J.E.; Stephens, R.S.
J. Bacceriol. 171, 285-291, 1989
A;Title: Identification by sequence analysis of two-site posttranslational processing c A;Reference number: A32244; MUD:89123030; PMID:2914847
A;Aocession: A32244
A;Aocession: A32244
A;Molecule type: DNA
A;Residues: 1-547 <ALL>
A;Coss-references: UNIPROT:P21354; GB:M23001; NID:g144552; PIDN:AA23152.1; PID:g14455
A;Coss-references: UNIPROT:P21354; GB:M23001; NID:g144552; PIDN:AA23152.1; PID:g14455
A;Coss-references: UNIPROT:P21354; GB:M23001; NID:g144552; PIDN:AA23152.1; PID:g14455
A;Note: parts of this sequence, including the amino ends of the precursor and mature p: R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect: Immun. 59, 1186-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton, Reference number: A3584; MUD:91147205; PMID:1997423
A;Residues: 1-547 <ADEL>
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A30472
A; Molecule type: DNA
A; Molecular cloning and sequence analysis of a developmentally regulated cystein
A; Molecular cloning and sequence analysis of molecular cloning and sequence pwiD:3066701
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C;Species: Chlamydia trachomatis
C;Date: 05-Dec-1998 #sequence revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: B43584; S13120; $18979; S24275
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1196-1201, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Description: associated with differentiation of reticulate bodies into elementary bod A;Note: essential for the structural integrity of the outer envelope of the elementary C;Superfamily: 60K cysteine-rich outer membrane protein C;Keywords: membrane protein; virulence C;Keywords: membrane protein; virulence P;1-22/Domain: signal sequence #status predicted ASIG> P;23-40/Domain: propeptide #status experimental <PRO> P;41-547/Product: 60K cysteine-rich outer membrane protein 2 #status experimental <PAMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmentally regulated trans
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A;Cross-references: GB:M35148; NID:g144485; PIDN:AAA23119.1; PID:g144487
A;Experimental source: serotype L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Pred. No. 36;
1; Mismatches 2; Inde
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A; Residues: 294 402 < wAH>
A; Resperimenta Source: serotype L2
R; Lambden, P.R.; Everson, J.S.; Ward, M.E.; Clarke, I.N.
Gene B7, 105-112, 1990
A; Title: Sulfur-rich proteins of Chlamydia trachomatis:
A; Reference number: JQ0514; MUID: 90236284; PMID: 2332164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.18;
72.78;
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159 GKLVWKIDRLG 169
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hes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JT0419
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C; Function:
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Best Local S
Matches
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                  A;Cross-references: UNIPROT:P30281; GB:M90814; NID:g180002; PIDN:AAA51927.1; PID:g180003 A;Note: sequence extracted from NCBI backbone (NCBIN:109687, NCBIP:109688)
R;Mote: sequence extracted from NCBI backbone (NCBIN:109687, NCBIP:109688)
B;Did:Chem. 267, 20412-20415, 1992
A;Title: Cloning and characterization of human cyclin D3, a cDNA closely related in sequal A;Reference number: A44022; MUID:9301592; PMID:1383201
A;Molecule type: mRNA
A;Molecule type: mRNA
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-354 <LEE>
A;Cross-references: UNIPROT:P18407; GB:J02927; NID:g168748; PIDN:AAA33556.1; PID:g168749
A;Note: the authors translated the codon TCC for residue 42 as Leu, CTG for residue 140
C;Superfamily: Allantoicase
C;Keywords: hydrolase
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                                                                                                                                                                                                                                                                                         C;Species: Neurospora crassa
C;Date: 30-Nov-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
C;Accession: A35829
R;Lee, H.; Fu, Y.H.; Marzluf, G.A.
Bjochemistry 29, 8779-4787, 1990
A;Tille: Nucleotide sequence and DNA recognition elements of alc, the structural gene valeference number: A35829; MUID:91104776; PMID:2148685
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C;Date: 12-Oct-1989 #sequence revision 27-Jun-1994 #text change 09-Jul-2004
C;Accession: A32244; A43584; Ā36043; A30472; JT0419; S18981; S24277
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64.3%; Pred. No. 15;
iive 2; Mismatches
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A,Introns: 66/3, 138/3; 192/1
A,Note: introns line may be incomplete
C,Superfamily: cyclin, A/B/D/E type
C,Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWEVLVLGKLKWDL 152
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Best Local Similarity 30.4
Matches 7; Conservative
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nes 9; Conserv
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Matches
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Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72.7%;
Matches 8; Conservative
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166 GKLVWKIDRLG 176
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A; Residues: 1-556 < ARN>
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A;Residues: 1-554 <T
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R, Stephens, R. S. J. Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A, Filtel e Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, A. Accession: D71515

A, Accession: D71515

A, Residues: 1-553 - ARR
A, Residues: 1-553 - ARR
A, Residues: 1-553 - ARR
A, Residues: L. Sequence diversity D, Strain UW-3/Cx

R; de la Maza. L. M.; Fielder T. J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect: Immun. 59, 1156-1201, 1991

A, Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton A, Residues: 7-238, VV, 240-553 ADEL>
A, ACCession: C43584
A, Rocession: C43584
A, 
A; Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton A; Reference number: A43584; MUID:91147205; PMID:1997423
A; Reference number: A43584; MUID:91147205; PMID:1997423
A; Recession: B43584
A; MUID:91147205; PMID:1997423
A; Residues: 1-547 < DEL.
A; Reference number: 18, 6713, 1990
A; Title: The nucleotide and derived amino acid sequence of the omp2 gene of Chlamydia tr A; Reference number: S13120; MUID:91067486; PMID:2251143
A; Reference number: S13120; MUID:91067486; PMID:2251143
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, 'S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, S', 459-547 < COL.>
A; Residues: 1-22, FF', 33-120, L', 122-131, A', 133-457, S', 459-547 < COL.>
A; Residues: 133-130, MID:340724; PIDN:CARA33396.1; PID:340725
A; Residues: 133-130, MID:340724; PIDN:CARA33396.1; PID:340725
A; Residues: 133-130, MID:340724; PIDN:CARA33396.1; PID:340725
A; Residues: 133-130, MID:340724; PIDN:CARA33396.1; PIDN:CARA33396.1; PID:340725
A; Residue: 133-130, MID:340724; PIDN:CARA33396.1; PIDN:CARA33396.1; PIDN:
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A;Gene: omp2; omcB
C;Function:
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60K cysteine-rich outer membrane protein precursor [similarity] - Chlamydophila pneumon C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (cjpate: 30-Sep-1993 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Accession: $12602; #72063; #780604 B;Watson, M.W.; Al-Mahdawi, S.; Lamden, P.R.; Clarke, I.N. Nucleic Acids Res. 18, 5299, 1990 A;Title: The nucleotide sequence of the 60kDa cysteine rich outer membrane protein of C A;Reference number: $12602; MUID:9034850; PMID:2402463
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A;Residues: 1-556 <WAT>
A;Cross-references: UNIPROT:P23700; GB:X53511; NID:9550564; PIDN:CAA37590.1; PID:955056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Chlamydia muridarum, Chlamydia trachomatis Mobn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81671
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
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A;Experimental source: strain Nigg (MoPn)
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R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A,Note: essential for the structural integrity of the outer envelope of the elementary C,Superfamily: 60K cysteine-rich outer membrane protein C,Keywords: membrane protein, virulence F;1-28/Domain: signal sequence #status predicted <SIG> F;2-46/Domain: propeptide #status predicted <PRO> F;29-46/Domain: propeptide #status predicted <PRO> F;47-553/Product: 60K cysteine-rich outer membrane protein 2 #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 kDa outer membrane protein TC0727 [imported] - Chlamydia muridarum (strain Nigg)
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                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Length 553;
Pred. No. 36;
1; Mismatches 2; Indels
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Pred. No. 36;
1; Mismatches
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us-10-092-750-49.rpr

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Search completed: November 10, 2004, 14:52:18 Job time : 5.41509 secs
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[c]species: Chlamydophila pneumoniae, Chlamydia pneumoniae
[c]ate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
[c]Accession: A86560
[R]Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
[A]Shirai, M.; Ailakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
[A]Fitle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
[A]Riference number: A86491; MUID:20330349; PMID:10871362
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-556 <STO>
A; Cross-references: UNIPROT: P23700; GB: BA000008; NID: G8978928; PIDN: BAA98763.1; GSPDB: GNA
A; Experimental source: strain J138
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-556 <REA>
A; Residues: 1-556 <REA>
A; Residues: 1-556 <REA>
A; Residues: 1-556 <REA>
Cross-references: GB: AE002180; GB: AE002161; NID: g7189117; PIDN: AAF38068.1; PID: g718912
A; Experimental source: strain AR39, HL cells
C; Comment: This protein is associated with the differentiation of reticulate bodies into It may also be an important virulence factor.
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(S.)Species: Arabidopsis thaliana (mouse-ear oress)
(S.)Species: Arabidopsis thaliana (mouse-ear oress)
(S.)Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
(S.)Accession: T48012
(S.)Accession: T48012
(S.) Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, February 2000
(A.)Reference number: Z24482
(A.)Accession: T48012
(A.)Accessi
                                                A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C)Genetics:
A)Gene: omcB; CP0195
C)Superfamily: 60K cysteine-rich outer membrane protein
C)Superfamily: 60K cysteine-rich outer membrane protein
C)Keywords: membrane protein; virulence
E)1-22/Domain: signal sequence #status predicted <SIG>
E)23-40/Domain: propeptide #status predicted <PRO>
E)23-40/Domain: propeptide #status predicted <PRO>
E)41-556/Product: 60K cysteine-rich outer membrane protein #status predicted <PAT>
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Pred. No. 36;
1; Mismatches 2; Indels
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Pred. No. 36;
1; Mismatches 2; Indels
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A;Cross-references: UNIPROT:Q9M1Q4; EMEL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
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C,Superfamily: 60K cysteine-rich outer membrane protein
Acids Res. 28, 1397-1406, 2000
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Best Local Similarity 72.7%;
Matches B; Conservative
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Best Local Similarity 72.7
Matches 8, Conservative
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0
                                              Score 45; DB 2; Length 673;
Pred. No. 45;
4; Mismatches 5; Indels
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                                                                                                                   1 DWQVLLGKLLWKIDNP 16
                                              Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
A;Introns: 99/1; 605/2
A;Note: T17J13.160
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:38:57; Search time 23.9774 Seconds (without alignments) 431.938 Million cell updates/sec Run on:

US-10-092-750-49 102 1 DWQVLLGKLLWKIDNPGI 18 Title: Perfect score: Sequence:

1825181 segs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		caenorhabdi	arabidopsis	lactococcus	schistosoma	schistosoma	caenorhabdi	agrobacteri	agrobacteri	debaryomyce	xanthomonas	xanthomonas	leishmania	bacteroides	corynebacte	rynebac	oryza sativ	homo sapien	paramecium	chlamydophi	chlamydophi	bordetella	bordetella	musculu	s muscu	neisseria m	chlamydophi	sapien	sapien	89 homo sapi	opirell	chlamydophi
	Description							7d1v9							Q8nls8 cory	œ							Q7wfi2 bord	Q9d099 mus musculu	Bac38101 mu	Q9jyl8 neis		Q8nef8 homo	in	Bad18589 homo		Q9zaw0 chla
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	ID	076432	Q9FNP6	Q9CFF1	Q9TYH3	Q9TYH4	022901	Q7D1V9	Q8UIQ4	Q6BW53	Q8PDP2	OBPOL6	095287	Q89ZE9	Q8NLS8	CAF20884	Q7XIX3	Q9H0J4	Q6BFHS	246163	046165	Q7VT35	Q7WFI2	APHC_MOUSE	BAC38101	Q9JYL8	Q9X4I1	Q8NEF8	Q6ZMY6	BAD18589	Q7UJP9	O9ZAW0
	BB :	7	7	~	N	0	7	N	~	0	N	N	N	(1	N	~	N			0					N	N	0	7	N	N	7	7
•	Length	309	966	207			257	258	290	352	387	389	1864	296	474	474	652	1663	2314	178	178	212	212	267	267	275	395	426	472	472	481	534
	Match	50.0	50.0	49.0	48.0	•	47.1	47.1	47.1	47.1	47.1	47.1	47.1	46.1	46.1	46.1		46.1	46.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1
	Score	51	51	20	4	49	48	48	48	48	48	48	48	47	47	47	47	47	47	46	46	46	46	46	46	46	46	46	46	4	46	46
Result	No.	н	7	m	4	ιΩ	9	7	ω	σ	10		12	13	14		16	17	18	49	20	21	22	23	24	25	56	27	28	20	30	31

Q6k9ul oryza sativ Q7m31 gloeobacter Q7puga anopheles g P30281 homo sapien Q02664 podospora a Q9af182 chlamydia s Q9af10 chlamydia p Q61ch5 chlamydia p Q61ch5 chlamydia p Q61ch5 chlamydia p Q6fn02 candida gla Q9s6b3 chlamydia p Q9s6b3 chlamydia p Q9s6b3 chlamydia p Q9s6b3 chlamydia p Q9s6b3 chlamydia p Q9s6b3 chlamydia p	
06K9U1 07NN31 07NN31 07D09 07D03 09AF82 09AF82 09AF82 09AF82 09AF83 06FCH3 06FNU2 095GB3 095LM3	
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658 19485 19485 2922 173 173 183 183 395 410 500	
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## ALIGNMENTS

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PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6183;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Q9TYH3
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Matches
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Q9TYH4
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorckin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. II.
Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006696; BAB10381.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:000576; F:nucleus; IEA.
InterPro; PR007791; DN537.
InterPro; IPR0077087; Zif CH2.
InterPro; IPR007604; Zif CH2.
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Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                     Emb|CAB71880.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
Tabata S.;
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50.0%; Score 51; DB 2; Length 309; ilarity 40.0%; Pred. No. 12; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 51; DB 2; Length 996; 56.2%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZĪNC FINGER C2H2 1; 4.
; 111222 MW; C824826A49AD7515 CRC64;
                                                                                                                                                                                                                                                                                    01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                             996 AA
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                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00355; ZnF C2H2; 5.
SMART; SM00451; ZnF U1; 4.
PROSITE; PS00028; ZINC_FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DWOVLLGKILWKIDNP 16
                                                                                                                 :| ::| :||::|:
258 EWMIVLAQLLWQLDH 272
                                                                                          1 DWQVLLGKLLWKIDN 15
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                                                                                                                                                                                                                                             PRELIMINARY;
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Pfam; PF00096; zf-C2H2; 1
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Best Local Similarity
Matches 9; Conserv
    Query Match
Best Local Similarity
Matches 6; Conserv
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 13, Last sequence update)
Serine protease SmSP1 light chain (Fragment).
Schistosoma manson; (Blood fluke).
Ebuaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosomat.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 15, Last sequence update)
Serine protease SmSP1 (Fragment).
Schistosoma mansoni (Blood fluke).
Elwaryota, Mecazca; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae; Schistosomat.
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Similarity 47.1%; Pred. No. 19,
8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                Length 207;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006383; AAK05625.1; -.
PIR; G86815; G86815.
Complete Protecome.
SEQUENCE 207 AA; 23410 MW; B4EBE03A872746A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004231; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:trypsin activity; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Peptidase S1A.
                                                                                                                                                                           Query Match
49.0%; Score 50; DB 2;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp.SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Protease; Serine protease.
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                                                                                                                                                                                                                                                                                                                        57 DWQELLQKSDWVIDAVGI
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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198 EWIIVLAQLLWQLDH 212
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                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
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05-JUL-2004
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Matches
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Q8UIQ4
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea;
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                     Cocude C.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
L. SIMILARITY: Belongs to peptidase family S1.
EMBL; AJ011561; CAA06691.1; -.
EMBL; AJ011561; CAA06691.1; EA.
GO; GO:0004295; Fitypsin activity; IEA.
EMCOPTO: IPRO002172; LDL. receptor A.
InterPro: IPRO01272; LDL. receptor A.
InterPro: IPRO01274; Peptidase S1A.
InterPro: IPRO01314; Peptidase S1A.
InterPro: IPRO0131; CUB; 1.
R. FAMNTS; RM00122; CHYMOTRYPSIN.
R. SMART; SM00122; LDLa; 1.
R. SMART; SM00125; LDLa; 1.
R. SMART; SM00120; LDLA; 1.
R. SMART; SM00120; TRYPSIN, 1.
R. PROSITE; PS501040; TRYPSIN, 1.
R. PROSITE; PS501040; TRYPSIN, 1.
R. PROSITE; PS50134; TRYPSIN, 1.8; UNKNOWN, 1.
R. PROSITE; PS00134; TRYPSIN, 1.8; UNKNOWN, 1.
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STRAIN=Bristol N2;
Gattung S., Le T.T.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 AA; 55029 MW; 29F26792C2014FA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C16D9.7.
ORFNames=C16D9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 48.0%; Score 49; DB 2; Local Similarity 47.1%; Pred. No. 41; les 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Protease, Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 WNCIMGKRLCKTRNPGV 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WOVLLGKLLWKIDNPGI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2; Waterston R.;
                                                            SEQUENCE FROM N.A. STRAIN-porto Rico;
NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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RESULT 6

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STRAINS-Cereon;

XX MEDLINE-21608551; PubMed=11741194;

XA Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

A qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Aurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

A purollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

XA Linger M., Doughty D., Scott C., Lappas C., Markelz B.,

R lanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

XA Cielo C., Slater S.;

T "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

T "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

Agrobacterium tumefaciens C58.";

LI STMILARITY: Concains 1 HTH arac/xyls-type DNA-binding domain.

EMBL; AS007963; AAR66055.1;

InterPro, IPRO0005; HTHARAC.

PRIMISSI ARC Landing; 1.

PRIMISSI PRO0003; HTHARAC.

PRIMISSI PRO0003; HTHARAC.

PRIMISSI PRO0003; HTHARAC.

PRIMISSI PRO0003; HTHARAC.

PRIMISSI PRO0003; HTHARAC.
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OrderediocusNames=AGR C 407;

Agrobacterium tumefaciens (strain CS8 / ATCC 33970).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

NCBI_TaxID=176299;
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                                                                                                                                                                                                                                                                                                                                                    Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                 (AUG-2003) to the EMBL/GenBank/DDBJ databases.
Wilson R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL; UG6858; AAB18286.2; -.
PIR; T29556; T29556.
WormPep; C16D9.7; CE06843.
InterPro; IPR002651; DUF32.
Ffam; PF01748; DUF32; 1.
Hypothetical protein.
SEQUENCE 257 AA; 29578 MW; B2784689FA6664CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D6D0256E4D65225 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    Query Match 47.1%; Score 48; DB 2; Best Local Similarity 40.0%; Pred. No. 31; Matches 6; Conservative 7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO0342; HTH_ARAC; 1.
PROSITE; PS01124; HTH_ARAC FAMILY 2; 1.
DNA-binding; Transcription regulation.
SEQUENCE 258 AA; 29109 WW; 3D6D02563
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387 AA
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Nature 417:459-463(2002).
Bell; AE012125; AAM9512.1;
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001910; I/U nuclsd_hydro.
ProDom; PD007736; I'U nuclydro; I.
ProDom; PD007736; I'U nuclsd_hydro; I.
Complete protecome; Hydrolase.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.3
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 430:35-44 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CBS767;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespam W., Perry M.,
Gordon-Kamm B., Lidao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Nester B.W.;
Mester B.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. Socience 294:2317-2323(2001).

1. Science 294:2317-2323(2001).

2. SIMILARITY: Contains 1 HTH araC/xylS-type DNA-binding domain.

BEMBL, AE008966; AAL41261.1; -.

PIR, AG2605; AG2605.

PIR, F97387; F97387.

R GO, GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:00055; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00305; HTHARAC.

R Ffam; PF02311, AraC binding; 1.

P Ffam; PF02311, AraC binding; 1.

P Ffam; PF0242; HTH ARAC.

R SMART; SMO032; HTHARAC.

CM PRINTS; PR00324; HTHARAC.

CM COMPLETE PS01124; HTH ARAC; 1.

CM COMPLETE PS01124; HTH ARAC; 1.

CM COMPLETE PS01124; HTH ARAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence hansenii.
0RPNames-DEHA0B143779;
0RPNam
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                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
12-MAR-2004 (TrEMBLrel. 26, Last annotation update)
13-MAR-2004 (TrEMBLrel. 26, Last annotation update)
13-MAR-2004 (TrEMBLrel. 26, Last annotation update)
14-MAR-2004 (Extrain CS8 / ATCC 33970).
15-MAR-2004 (Extrain CS8 / ATCC 33970).
15-MAR-2004 (Extrain CS8 / ATCC 33970).
15-MAR-2004 (Extrain CS8 / ATCC 33970).
16-MAR-2004 (Extrain CS8 / ATCC 33970).
17-MAR-2004 (Extrain CS8 / ATCC 33970).
18-MAR-2004 (Extrain CS8 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.1%; Score 48; DB 2; Length 290; Best Local Similarity 60.0%; Pred. No. 35; Matches 9; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA.
290 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Dupont;
MEDLINE=21608550; Pubmed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 DWOSRLSDLLWKHSN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DWQVLLGKLLWKIDN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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GENOLEVURES;
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QEBW53; Q6BW53

RESULT 9 Q6BW53

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REQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAIN-ATCC 33913 / NCPPB 528;

RAM MEDINE-2020145; Probred J.A., Rethach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C., Ferro J.A., Rethach F.C., Camargo L.B.A.,

RA dueggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Carelli R.M.B., Coulinho L.L., Cursino-Santos J.R., Clapina L.P.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Ratsuyama A.M., Kishi L.T., Lette R.P., Lemos B.G.M., Lemos M.V.F.,

RASTINS C., Machadon M.A., Madeira A.M.B.N., Martine Z., Moron D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira W.R.,

Spinola L.A.F., Tarkita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.F., Tarkita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

T. Comparison of the genomes of two Xanthomonas pathogens with differing
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Antraper F., Hennequin C., Jauniaux N., Joyer P., Kachouri R., Karreet A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., A. Sellenz S., Potier S., Richard G.F., Streub M.L., Suleau A., Swennene D., Tekala F., Wesclowski-Louvel M., Westhof E., With B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Mincker P., Souciet J.L., Scarpelli C., Gaillardin C., Weissenbach J., Wichene evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae; Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%; Score 48; DB 2; Length 352; 35.3%; Pred. No. 42; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope;
Submitrted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382134; CAGB5577.1; -.
SEQUENCE 352 AA; 40083 MW; 40505E557CC2F7EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.

RESTRAIN-VPI-5482 / ATCC 29148;

RX MEDLINE=2255088; PubMed=12663928;

RX MEDLINE=2255088; PubMed=12663928;

RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;

RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

RI Science 299:2074-2076(2003).

DR EMBL, ABO16945; AAA79533.1;

DR EMBL, ABO16945; AAA79533.1;

Complete proteome; Hypothetical protein.

KW Complete proteome; Hypothetical protein.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
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EMBL; AL389894; CAC44916.1; -.
                                                                                                                            STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
Ivens A., Chan E., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1864;
                                                                                                                                                                                                                               "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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Q1-QCT-2002 (TrEMBLrel. 22, Created)
01-QCT-2002 (TrEMBLrel. 22, Last sequence update)
01-QCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical membrane protein (Putative membrane protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1864 AA; 201407 MW; C999DB258BD104E3 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%; Score 48; DB 2; Le
43.8%; Pred. No. 2.4e+02;
ive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1815 WOLLAGAKVWRFMDPG 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteroides thetaiotaomicron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WQVLLGKLLWKIDNPG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
OrderedLocusNames=BT4428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65...
Triangle Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002110; ANK.
PRINTS; PR01415; ANKYRIN.
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168 GKVVWKLDVPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 1864 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 7; Conserv
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               STRAIN=Friedlin;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q89ZE9;
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                       Length 387;
                                                                                                                            Indels
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            42450 MW; 44684F6D4093D4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein LT.09.
Name-LT.09; Synonyms-P131.01;
Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.1%; Score 48; DB 2; 63.6%; Pred. No. 47;
                                                                       ..
73
                                                           DB 7
                                                                 Score 48; DB 2
Pred. No. 47;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              389 AA
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                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                    47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=XAC0307;
                                        Query Match
Best Local Similarity 63.0
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.6 es 7; Conservative
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                                                                                                                                                                                       2 WOVLLGKLLWK 12
                                                                                                                                                                                                                            88 WEALYGKLVWK 98
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Nucleoside hydrolase.
            387 AA;
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            SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesnann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHARICY A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Tauch A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
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Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Tauch A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins."; up 104:5-25(2003).

EMBL; APO05283; BAC00253.1; -.

EMBL; APO05283; BAC00258.1; -.
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J. Biotechnol. 104:5-25(2003).
EMBL: BX927156; CAP20884.1; -.
SEQUENCE 474 AA; 50594 WW; 3810825D5298DDB3 CRC64;
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OrderedLocusNames=Cg12859, cg3165;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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46.1%; Score 47; DB 2; Length 474;
Best Local Similarity 64.3%; Pred. No. 84;
Matches 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amatch
Local Similarity 64.3%; Pred. No. 84;
Los 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
Nakagawa S.;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Putative membrane protein.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                      NCBI_TaxID=1718;
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CAF20884;
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Matches
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Search completed: November 10, 2004, 14:50:08 Job time: 25.9774 secs

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TOPOLOGY: linear
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US-08-378-761A-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71, Appl
Sequence 71, Appl
Sequence 3, Appli
Sequence 862, Appl
Sequence 862, Appl
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Sequence 2, Appli
Sequence 26931, A
                                                                                                                                                              November 10, 2004, 13:44:14; Search time 8.05283 Seconds (without alignments) 181.178 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/i/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/i/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/i/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/i/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/i/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/i/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-378-761A-71

US-08-485-286-71

US-09-489-034A-9109

US-09-489-034A-9109

US-09-134-000C-525

US-09-134-000C-525

US-09-134-000C-525

US-09-134-000C-525

US-09-538-092-249

US-09-581-110-3642

US-09-581-110-3642

US-09-582-26-2

US-09-052-262-2

US-09-052-262-8

US-09-052-263-8

US-09-052-263-8

US-09-052-263-8

US-09-052-263-8

US-09-052-263-8

US-09-052-263-8

US-09-252-991A-31694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                        478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                  111
1 GAMEREWAMFLRAASSRIRGGV 22
                                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg length: 0
seg length: 200000000
                                                                                                                                                                                                                                                          US-10-092-750-50
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                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Maximum DB
                                                                                                                      OM protein
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                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                   Run on:
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GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMONIN D

APPLICANT: HORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: ANDREA T: BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                      Sequence 25754, Ascience 3, Appli
Sequence 31782, A
Sequence 8306, Ap
    Sequence 27468, A
Sequence 21750, A
Sequence 2180, A
Sequence 12633, A
Sequence 19788, A
Sequence 2, Appli
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COMPUTEX: US

ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSITICATION NUMBER: 33631
ATTORNEY/AGNT INFORMATION:
NAME: BORGUKI, ANDREA T
REGISTRATION NUMBER: 33631
FELERENCE/DOCKET NUMBER: 33631
FELERENCE/DOCKET NUMBER: 33631
FELERENCE CHARACTERISION:
TELERENCE CHARACTERISION:
SEQUENCE CHARACTERISITICS:
LENGTH: 250 and no ocide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: SEQUENCE CHARACTERISION:
TYPE: AMINO ACIDE
TYPE: AMINO
US-09-252-991A-27468
US-09-252-991A-28750
US-09-252-991A-32633
US-09-252-991A-32633
US-09-248-756A-19788
US-08-188-582-2
US-08-188-582-2
US-09-252-991A-25754
US-09-252-991A-25754
US-09-252-991A-25754
US-09-252-991A-25754
US-09-252-991A-25754
US-09-252-991A-25754
US-09-246-969-3
US-09-246-969-3
US-09-246-969-3
US-09-246-969-3
US-09-247-267-3
US-09-247-267-3
US-09-249-0928-306
US-09-891A-31782
US-09-8918-306
US-08-981-785A-10
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41.4%; Score 46; DB 1
Best Local Similarity 36.4%; Pred. No. 7.4;
Matches 8; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 71, Application US/08378761A; Patent No. 5635384
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Gaps

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Sequence 9109, Application US/09489039A

Sequence 9109, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEBIELIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 9109

LENGTH: 151

TYPE: PRI
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; Sequence 862, Application US/09538092
; Patent NO. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15866-54
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 862
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41.4%; Score 46; DB 4; Length 251;
Best Local Similarity 36.4%; Pred. No. 7.5;
Matches 8; Conservative 5; Mismatches 9; Indels
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39.6%; Score 44; DB 4; Length 151;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 8; Conservative 3; Mismatches 5; Indels
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LOCATION: (0)...(0)

CTHER INFORMATION: Polypeptide Accession Number P07029

US-09-538-092-86
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; EARLIER FILING DATE: 1999-03-30; NUMBER OF SEQ ID NOS: 19; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 3; LENGTH: 251; TYPE: PRT CRGANISM: Abrus precatorius US-09-538-873-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Klebsiella pneumoniae US-09-489-039A-9109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 REWAMFLRAASSRIRG 20
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                                                                                                                                              Sequence 71, Application US/08485286

Sequence 71, Application US/08485286

Patent No. 5646026

TITLE OF INVENTION: TRESONE-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR-INACTIVATING PROCESS FOR MAKING A METHOD OF

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: ANDREAT: BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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US-09-538-873-3

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

SET OF USE OF US
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SIALE: 10

SIP: 4626B FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION NUMBER: US/08/485,286
FILING DATE:
PRICK APPLICATION NUMBER: US/08/485,286
TILING DATE: 26-JAN-1995
ATFORNEY/AGENT INPORMATION:
NAME: BORUCKI, ANDREA T
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OF 71:
SEQUENCE CHRARACTERISTICS:
LENTH: 250 cmino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-485-286-71
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                                                                                           RESULT 2
US-08-485-286-71
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Gaps

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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 1996-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURRENTHER CURRENTER CONTRACTOR OF SEQ ID NOS: 1387
SOFTWARE: CURRENTHER CURRENTER CONTRACTOR OF SEQ ID NOS: 1387
SOFTWARE: CURRENTER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

: LOCATION: (0)...(0)

: OTHER INFORMATION: Polypeptide Accession Number YER102W

US-09-538-092-249
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COMPUTER: IBM Compatible
COMPATION SYSTEM: DOS
SOFTWARD: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: US/08/858,207A
FILING DATE: US/08/858,207A
FILING DATE: 14-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT THORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 301, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 98,891
TELECOMMUNICATION INFORMATION:
Sequence 249, Application US/09538092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 ERKWA--ARAASAKIESSV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 EREWAMFLRAASSRIRGGV 22
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52.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ACID ACID ACID ACID AND THERAPEUTICS
CURRENT PAPELICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/00/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22829
LENGTH: 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parente 2553, Application US/09134000C

parente 2523, Application US/09134000C

parente No. 6617156

GENERAL INFORMATION:

parente No. 6617156

GENERAL INFORMATION:

parente OF INVENTION:

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                                            Score 43; DB 4; Length 225; Pred. No. 21;
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                                                                                                                                 7; Indels
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Pred. No. 27;
4; Mismatches
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-22829

Sequence 22829, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 MEREWAMFL----RAASS---RIRG 20
                                                                                                                                                                                                                                                                  90 AQREEWKMFIRALAGTLQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                             2 AMEREWAMFLRAASSRIR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557 REWAVFLRRVFQHAHG 572
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                                   Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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Best Local Similarity 44.0%;
Matches 11; Conservative
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US-09-134-000C-5253
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US-09-538-092-249
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Query Match 37.8%; Score 42; DB 4; Length 1464; Best Local Similarity 43.8%; Pred. No. 2.5e+02; Matches 7; Conservative 3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09052469
Patent No. 6380360
GENERAL INFORMATION: POYECTE KIDNEY DISEASE 1 GENE TITLE OF INVENTION: POYECTE KIDNEY DISEASE 1 GENE TITLE OF INVENTION: POYECTE 23
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 120 PC COMPUTED: COMPUTER: WORDPER: US/09/052,469 FILING DATE: WORDPER: US/09/052,469 FILING DATE: 14-April-1995 PRIOR APPLICATION NUMBER: 08/422,582 PRIOR APPLICATION NUMBER: 08/422,582 PRIOR APPLICATION NUMBER: GB 9507766.5 PRIOR APPLICATION NUMBER: GB 9507766.5 PRIOR APPLICATION NUMBER: GB 9411900.5 PRIOR APPLICATION NUMBER: GB 9411900.5 FILING DATE: 14-JUN-1994 PRIOR APPLICATION NUMBER: GB 926470.3 ATTORNEY/GRATION NUMBER: GB 9326470.3 ATTORNEY/GRATION NUMBER: BB 9336470.3 ATTORNEY/GRATION NUMBER: 34,380 REPERENCE/DOCKET NUMBER: 34,380 REPERENCE/DOCKET NUMBER: 3265/74165 TELECOMMUNICATION NUMBER: 3265/74165 TELECOMMUNICATION NUMBER: 3265/74165 TELECOMMUNICATION NUMBER: 3265/74165
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1188 GAADRQWTRFVRGRPRR 1204
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925 DNHWALFAKAVLDRIR 940
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                                                                                                                        4 EREWAMFLRAASSRIR 19
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TELEFAX. (617) 345-9111
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                      RESULT 12
US-09-052-469-2
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## Sequence 2. Application US/10038224

## Patent No. 6734340

## GENERAL INFORMATION

## APPLICATION Schewe et al.

## TITLE OF INVENTION: Monocotyledon plant cells and plants which synthesise modified st

## FILE REFERENCE: 514413-3900

## CURRENT APPLICATION NUMBER: US/10/038,224

## CURRENT APPLICATION NUMBER: US 10052492.3

## PRIOR PLING DATE: 2000-10-23

## PRIOR PLING DATE: 2000-12-22

## PRIOR PLING DATE: 2000-12-22

## PRIOR FILING DATE: 2000-12-22

## PRIOR PRIOR PRIOR DATE: 2000-12-22

## PRIOR FILING DATE: 2000-12-22

## PRIOR PRIOR DATE: 200
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                                                                                                                                                                                                                                                                      Length 671;
                                                                                                                                                                                                                                                                                                                              6; Indels
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37.8%; Score 42; DB 3; I
Best Local Similarity 35.3%; Pred. No. 1.1e+02;
Matches 6; Conservative 5; Mismatches 6
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      INFORMATION FOR SEQ ID NO: 301:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acids
STRANDEDNESS: single
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189 EKRWSIFLRPVGEDLKG 205
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                                                                                                                                                                                                                                                                                                                                                                                            4 EREWAMFLRAASSRIRG 20
                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-301
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Matches 6, Conservative
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37.8%; Score 42; DB 4; Length 161
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 7; Indels
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US-08-658-136-5
IS-08-658-136-5
| Sequence 5, Application US/08658136
| Patent No. 6071717
| GENERAL INFORMATION:
| APPLICANT: LANDES, GRECORY M
| APPLICANT: LANDES, GRECORY M
| APPLICANT: CONNORS, TIMOTHY C
| APPLICANT: GERMINO, GRECORY M
| APPLICANT: GERMINO, GRECORY M
| APPLICANT: GERMINO, GRECORY
| APPLICANT: GERMINO: GRECORY
| APPLICANT: GERMINO: GRECORY
| APPLICANT: GERMINO: GRECORY
| APPLICANT: GERMINO: STEATH OF THE ST
            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDITUM TYPE: Flopy disk, 3.50 inch
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,262

FILING DATE: 14-APPLICATION DATA:
APPLICATION NUMBER: 08/42,582

FILING DATE: 13-APPLICATION DATA:
APPLICATION NUMBER: GB 9411900.5

FILING DATE: 14-APPLICATION DATA:
APPLICATION NUMBER: GB 926470.3

FILING DATE: 24-DEC-1994

PRIOR APPLICATION NUMBER: GB 9326470.3

FILING DATE: 24-DEC-1994

PRIOR APPLICATION NUMBER: GB 9326470.3

FILING DATE: 24-DEC-1994

PRIOR APPLICATION NUMBER: BB 326470.3

FILING DATE: 34-DEC-1994

PRIOR APPLICATION NUMBER: BB 326470.3

FILING DATE: 34-380

REGREENCE/DOCKET NUMBER: 34-380

REGREENCE/DOCKET NUMBER: 34-380

REGREENCE/DOCKET NUMBER: BB 326470.3

TELEPAK: (617) 345-9100

TELEPAK: (617) 345-9100

TELEPAK: (617) 345-9101

INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1614 Amino acids

LENGTH: 1614 Amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAMEREWAMFLRAASSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-09-052-262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
   COUNTRY:
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      Sequence 2, Application US/09052262
Patent No. 6656681
GENERAL INFORMATION:
APPLICANT: Harris et al.
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
STREET: One Financial Center
CITY: Boston
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US-09-052-262-2
US-08-422-582-2
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OPERATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
TILING DATE:
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: LELZABEN: BILZABER: BILZABER:
TELECOMMONICATION NUMBER: 31,445
TELECOMMONICATION NUMBER: GEN4-17.8
TELECOMMONICATION NUMBER: GEN4-17.8
TELECOMMONICATION NUMBER: GEN4-17.8
TELECOMMONICATION NUMBER: GEN4-17.8
TELECOMMONICATION SOBERIALIZES:
TELECOMMONICATION SOBE
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RESULT 2
US-10-001-835-218
US-10-001-835-218
' Sequence 218' Application US/10001835
' Publication No. US20020160387A1
' GENERAL INFORMATION:
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270202,
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                                                                                                                                      November 11, 2004, 01:28:30; Search time 25.4453 Seconds (without alignments) 305.399 Million cell updates/sec
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(gnz 6/ptodata//pubpaa/USO6 FUBCOMB.pep:*

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(gnz 6/ptodata//pubpaa/USO7 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/USO8 PUBCOMB.pep:*

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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-001-835-218
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US-10-424-599-209333
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Listing first 45 summaries
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1 GAMEREWAMFLRAASSRIRGGV 22
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Sequence 3324., Apsequence 196344 bequence 196344 bequence 196344 bequence 34086; A Sequence 60544; A Sequence 5127829, Sequence 10620, A Sequence 10620, A Sequence 10620, A Sequence 128120, Sequence 179626, Sequence 147013; Sequence 243709, Sequence 147013; Sequence 263709, Sequence 147013; Sequence 263709, Sequence 147013; Sequence 263709, Sequence 147013; Sequence 263709, Sequence 263721, Se
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Hammond, Philip W.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1; FILE REFERENCE: 50036/050002; CURRENT APPLICATION NUMBER: US/10/092,750; CURRENT APPLICATION NUMBER: US/10/092,750; PRIOR PILING DATE: 2002-03-07; PRIOR FILING DATE: 2001-03-08; NUMBER: US SQI ID NOS: 253; SOFTWARE: FastSEQ for Windows Version 4.0; LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
6 US-10-425-115-325061
6 US-10-767-701-43701
6 US-10-282-122A-43701
6 US-10-437-963-108434
6 US-10-437-963-151413
7 US-10-437-963-154485
4 US-10-437-963-154485
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7 US-10-425-114-62544
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0; Mismatches 0;
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Best Local Similarity 100.0%;

Matches 22; Conservative 0;
     TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-50
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Sequence 224673, Application US/10425115

Sequence 224673, Application No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Last Sosa, Thomas J.
APPLICAMY: Last Sosa, Yound
APPLICAMY: Chou, Yihua
APPLICAMY: Chou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 224673
LENGTH: 204
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LOCATION: (65)..(65)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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COCATION: (165)...(165)
19 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-598
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42.8%; Score 47.5; DB 17; Length 204;
Best Local Similarity 48.0%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 6; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (43)..(44)
OTHER INFORMATION: Xaa can be any naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
43.7%; Score 48.5; DB 15;
Best Local Similarity 57.9%; Pred. No. 12;
Matches 11; Conservative 3; Mismatches 4;
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OTHER INFORMATION: Clone ID: MRT4577_13648C.1.pep
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR PILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PARENTIN VERSION 3.2
SEQ ID NO 958
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AAEREEVAWEWSRLLRSAVGRHRGG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa
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APPLICANT: Recipon, Herver

APPLICANT: Recipon, Herver

APPLICANT: Cafferkey, Robert

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro

FILE REPRENCE: DEX-0277

CURRENT PAPLICATION NUMBER: US/10/001,835

CURRENT FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/249,997

PRIOR PILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: PatentIn version 3.1

SEQ ID NO 218

TYPE

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| Sequence 1007, Application US/10001885
| Publication No. US20040058319A1
| CENERAL INFORMATION:
| APPLICANT: Salceda, Susana |
| APPLICANT: Recipon, Herve |
| APPLICANT: Recipon, Herve |
| APPLICANT: Cafferkey, Robert |
| APPLICANT: Liu, Chenghua |
| TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profunce: DEX-0279 |
| CURRENT APPLICATION NUMBER: US/10/001,885 |
| CURRENT APPLICATION NUMBER: 60/252,061 |
| PRIOR FILING DATE: 2000-11-20 |
| PRIOR FILING DATE: 2000-11-27 |
| PRIOR FILING DATE: 2000-11-27 |
| NUMBER OF SEQ ID NOS: 167 |
| SOFTWARE: PatentIn version 3.1 |
| SEQ ID NO 107 |
| LENGTH: 82
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Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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88.3%; Score 98; DB 13; Length 82
Best Local Similarity 90.9%; Pred. No. 6.2e-08;
Matches 20; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CORGANISM: Homo sapien US-10-001-835-218
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US-10-001-885-107
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US-10-389-566-958
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Sequence 3, Application US/10440796
Sequence 3, Application US/10440796
GENERAL INFORMATION:
APPLICANT: VITETA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: MALLSHAW, JOAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
CURRENT FALING DATE: 2003-05-19
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 3
FRANCE PLANCE TO SEQ ID NOS: 19
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALLUAR, ROXANA G.
TITLE OF INVENTION: COMFOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: US/10/282,935
CURRENT APPLICATION NUMBER: 08/528,873
PRIOR PLILING DATE: 2002-10-29
PRIOR PLILING DATE: 2000-03-30
PRIOR PLILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
SOFTWARE: PALENTIN VOY: 2.1
SEQ ID NO 3
LING APPLICATION 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 15;
Pred. No. 42;
5; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAMEREWAMFLRAASSRIRGGV 22
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Best Local Similarity 36.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Abrus precatorius
US-10-282-935-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Abrus precatorius
US-10-440-796-3
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US-10-440-796-3
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Sequence 209333, Application US/10424599

Publication No. US20040031072A1

Sequence 209333, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION

APPLICANT: La Rosa Thomas J

APPLICANT: About Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PLING DATE: 2003-04-28

SEQ ID NO 209333
                                                                                                                                                                                                                    and Other Molecules Associated With
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                   Sequence 270202, Application US/10424599; Sequence 270202, Application WS/10424599; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Assc;
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION WUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 270202
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Pred. No. 32;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
42.3%; Score 47; DB 15; Length 92;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT MRT3847_86010C.1.pep
US-10-424-599-270202
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US-10-424-599-209333
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LOCATION: (1)..(189)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AMEVEWKKIKRKAAARREGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AMEREWAMFLRAASSRIRGG 21
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68.8%; Pre
tive 0;
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Best Local Similarity 68.8<sup>§</sup>
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
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           US-10-424-599-270202
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US-10-282-935-3
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Sequence 263566, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF SEQUID NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263656
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US-10-425-115-325061

Sequence 325061, Application US/10425115

Sequence 325061, Application US/10425115

BUBLICARIE AR ROWALTON:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Tongwei T.
APPLICANT: Cao, Yongwei T.
APPLICANT: Cao, Yongwei T.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 325061
ENOUTH: 192
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; OTHER INFORMATION: Clone ID: PAT_MRI3847_80100C.1.pep
US-10-424-599-263656
                                                                                                      TYPE: PRT CRANISM: Zea mays PEATURE: PEATURE: O'REANTRE: D'THEORYATION: Clone ID: MRT4577_65144C.1.pep US-10-425-115-331184
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; ORGANISM: Zea mays
; FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_59526C.1.pep
US-10-425-115-325061
                                                                                                                                                                                                                                                        Query Match
40.5%; Score 45; DB 17;
Best Local Similarity 40.7%; Pred. No. 41;
Matches 11; Conservative 3; Mismatches 7.
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Pred. No. 15;
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CURRENT FILING DATE: 2003-04-28
WINDER FOF SEQ ID NOS: 369326
SEQ ID NO 331184
LENGTH: 170
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Best Local Similarity 47.4%;
Matches 9; Conservative '
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US-10-152-886-37

Sequence 37, Application US/10152886

Publication No. US20030064491A1

GENERAL INFORMATION:
APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: EARTHC, Chris
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
TITLE OF SEQ ID NOS: 102
CURRENT APPLICATION NUMBER: US/10/152,886
CURRENT APPLICATION NUMBER: US/10/152,886
CURRENT PILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 102

SEQ ID NO 37

LENGTH: 328

LENGTH: 328
                                                                                                   APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190381
LENGTH: A34
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Sequence 331184, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Evoalsc, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REPERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115
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41.0%; Score 45.5; DB 14; Length 328;
Best Local Similarity 32.4%; Pred. No. 67;
Matches 12; Conservative 5; Mismatches 5; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.4%; Score 46; DB 16; Length 434; Best Local Similarity 50.0%; Pred. No. 74; Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Streptomyces carzinostaticus neocarzinostaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_86801C.1.pep
US-10-437-963-190381
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  Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MEREWAMFLRAASSRIRG 20
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-152-886-37
                                 APPLICANT:
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RESULT 15
US-10-767-701-43701
Sequence 43701, Application US/10767701
Sequence 43701, Application US/10767701
Sequence 43701, Application VS/10767701
Sequence 43701, Devid K.
Sequence 43701
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Pred. No. 1e+02;
1; Mismatches 4; Indels
Query Match
39.6%; Score 44; DB 17; Length 192;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRANISM: Sorghum bicolor
FEATURE:
CHARLINFORMATION: Clone ID: SORBI-28MAY03-C13563_1.pep
US-10-767-701-43701
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Best Local Similarity 61.5%;
Matches 8; Conservative
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us-10-092-750-50.rpr

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(c) 1993 - 2004 Compugen Ltd.
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1 GAMEREWAMFLRAASSRIRGGV 22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	abrin (clone 7.2)	$\rightarrow$	hypothetical prote	aldolase Atulõ14 [	hypothetical prote	- 4	hypothetical prote	ρ.	heterogeneous ribo	GTP-binding protei	conserved hypothet	maltose ABC transp	- 2~	crumbs protein - f	ribosomal protein	probable transfera	hypothetical prote		괻	probable membrane	hypothetical prote	polycystic kidney	conserved hypothet	hypothetical prote	_	ㄷ	invertase, cell-wa	biotin carboxyl ca
SUMMARIES	ID	C84185	: C39761				G974B3	E6947											T01923								T2228		S25151	B5557
	Length DB	49	51	528 1	31	99													521 2								•			
de	Query	41.4	41.4	41.4	40.5	•	ö	σ.	φ.	38.7	38.7	38.7	38.7	38.7	8	8	7	7	37.8	7	7	7			ů.	Ġ	w	ú	36.9	ú
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A; Molecule type: DNA

probable serine/th probable RNA helic	cal		hypothetical prote	hemolysin A [impor	tRNA-pseudouridine	probable glycosyl	probable dTDPgluco	opsin - bluebottle	probable polygalac	hypersensitivity r	probable transmemb	hypothetical prote	abrin-b precursor	abrin-d precursor
A70652 B75633	T31604	E72730	529158	E87413	E83257	A69290	E95870	A39234	A96609	T45653	T35663	AC0675	832430	S32431
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1110	377	229	230	243	285	324	346	371	434	447	485	518	527	528
36.9	36.5	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0
	ı ıs	40	40	40	40	40	40	40	40	40	40	40	40	40
41	40.5	•												

### ALIGNMENTS

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Cispecies: Halobacterium sp. NRC-1
Cispecies: Garcession: G64185
RiNg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, i. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84185
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <STO>
C;Genetics:
A;Gene: VNG0250C
C;Superfamily: uncharacterized conserved protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dayiditatic (clone 7.2) precursor - Indian licorice (fragment)

N. Contains: rRNA N-glycosidase (EC 3.2.2.22)

C. Species: Abrus precatorius (Indian licorice)
C. Species: Abrus precatorius (Indian licorice)
C. Accession: C39761; S14471

R. Evensen, G.; Mathiesen, A.; Sundan, A.
U. Balo.: Chem. 266, 6848-6822, 1991
A. Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A. Reference number: A39761; MUID:91201329; PMID:2016300
A. Molecular C39761
A. Molecular UNIPROT:Q38760
A. Molecular UNIPROT:Q38760
A. Molecular Services and Captain A.; Sundan, A.
A. Residues: 1-251 cEVB>
A. Corss-references: UNIPROT:Q38760
A. Molecular Captain A.; Sundan, A.
A. Residues: 1-251 cEVB>
A. Corss-references: Mathiesen, A.; Sundan, A.
A. Molecular Caloning of two distinct abrin A-chains.
A. Molecular Captains.
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Llarity 63.2%; Pred. No. 5.6;
Conservative 2; Mismatches 3; Indels
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Les 12; Conserv
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A;Accession: S74110
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A;Accession: S74111
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A;Accession: S74111
A;Accession: S74111
A;Accession: S7411
A;Accive accession: Accession
B;Accession: Accession
B;Accession
B;A
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A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cjāccession: G83823
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
Nyaitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein BH1391 [imported] - Bacillus halodurans (strain C-125)
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C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                             A; Molecule type: protein
A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>
K; Lin, S. H.; Chow, L. P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 534-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110; WUID:97008945; PMID:8856055
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47.1%; Pred. No. 7.6;
iive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.4%; Score 46; DB 1; Length 528; ilarity 36.4%; Pred. No. 12; Conservative 5; Mismatches 9; Indels
A,Title: The complete primary structure of abrin-a B chain.
A,Reference number: S24133; MUID:92371656; PMID:1505674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAMEREWAMFLRAASSRIRGGV 22
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Conservative
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Best Local Similarity
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nes 8; Conserv
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A;Residues: 1-231 <STO>
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A; Status: preliminary
                                                                              A; Accession: S24133
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N; Contains: RRNA N-9Jycosidase (EC 3.2.2.2)

C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Date: 31-Dec-1933 #sequence revision 01-Aug-1997 #text_change 09-Jul-2004
C; Accession: S32429; JU2022; A33761; JC1399; S14472; S24133; S74110; S74111
R; Hung C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A; Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. CA A; Reference number: S32429; MUD:9313798; PMID:8421313
A; Accession: S33429
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 'E', 2-528 *HUN>
A; Cross-references: UNIPROT:P11140; GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A; Note: the coding region for the sequence shown is preceded by an ATG codon
A; Note: residues: 'E', 2-628 *HUN>
A; Note: residues: 'B, 'Emernosono, M:' Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
A; Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from A; Accession: JT0202
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C;Superfamily: ricin; rRNA N-glycosidase homology
C;Superfamily: ricin; rRNA N-glycosidase; hydrolase; lectin; toxin
F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;7-4,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
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                                                                                                                                                                                                                                                                                        41.4%; Score 46; DB 2; Length 251; ilarity 36.4%; Pred. No. 5.6; Conservative 5; Mismatches 9; Indels
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A; Residues: 'ME', 2-251 < EV2>
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Best Local Similarity
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A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae. A;Reference number: A69250; MUD:98049343; PMID:9389475
A;Accession: E69473
A;Reference number: A69250; MUD:98049343; PMID:9389475
A;Accession: E69473
A;Reference number: A69250; MUD:080484; GB:AE000979; GB:AE000782; NID:92689302; PIDN:AA8894
A;Rolecule type: DNA
A;Rolecule type: DNA
Cross-references: UNIFROT:028484; GB:AE000979; GB:AE000782; NID:92689302; PIDN:AA8894
C;Superfamily: DNA polymerase II small subunit, archaeal type; phosphoesterase core hom C;Keywords: metalloprotein; nucleotidyltransferase
F;228-326/Domain: phosphoesterase core homology <PEC>
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A,Status: presiminary
A,Molecule type: DNA
A,Residues: 1-154 «HEI»
A)Cross-references: UNIPROT:Q9KQ58; GB:AB004287; GB:AB003852; NID:g9656689; PIDN:AAF952
A)Cross-imental source: serogroup O1; strain N16961; biotype E1 Tor
A)Genetics:
A)Genetics:
A)Geneticon: 1
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C;Species: Genorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T15628
B;Johnson, D.
Submitted to the EMBL Data Library, June 1995
A;Bestiption: The sequence of C. elegans cosmid C25H3.
A;Reference number: Z18379
A;Reference number: Z18379
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule: type: DNA
A;Molecule: type: DNA
A;Residues: 1-1166 < JOH>
A;Residues: 1-1166 < JOH>
A;Residues: L1166 < JOH>
A;Residues: L1160 < JOH>
A;Re
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A;Gene: CESP:C25H3.9
A;Introns: 45/3; 82/3; 129/2; 180/2; 202/1; 215/3; 252/1; 374/3; 544/2; 1028/3; 1108/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%; Score 44; DB 1; Length 488; 38.9%; Pred. No. 23;
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243 LEKEWEMFVRWLKGEVGG 260
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Matches 7; Conserv
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aldolase Atulo14 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2701
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
KATP, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aritics: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

Aritics: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

Aritics: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

Aritics: Preliminary

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Aritics: C58.

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40.5%; Score 45; DB 2;
Best Local Similarity 52.4%; Pred. No. 8.7;
Matches 11; Conservative 3; Mismatches
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Pred. No.
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A;Map position: circular chromosome
C;Superfamily: 2,4-dihydroxyhept-2-ene-1,7
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Best Local Similarity 52.4%;
Matches 11; Conservative
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Pred. No.
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C, Superfamily: bcsA protein
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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;Status: preliminary
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H75603
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R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; C, Accession: B69669
R; Smith, D.R.; Doucette-Stamm, L.A.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Xi, C, Luch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J, Bacteriol. 179, 7135-7155, 1997
A; PMID: 9371463
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Residues: 1-399 cMTH>
C; Genetics:
A; Coss-references: UNIPROT: 027559; GB: AE000912; GB: AE000666; NID: G22622632; PIDN: AAB8599
A; Externated source: strain Delta H
C; Genetics:
A; Gene
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Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
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Best Local Similarity 50.0%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 6. Tradele
        Length 154;
                                                                                                                                                                                                                                                                                                          heterogeneous ribonuclear particle protein C - human (fragment)
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                                                               Indels
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     Query Match
Best Local Similarity 44.4%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches
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Pred. No. 16;
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27 INRAWVMFVMAGVSREOG 44
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                                                                                                                     3 MEREWAMFLRAASSRIRG
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Best Local Similarity
Matches 7; Conserv
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AG3170 conserved hypothetical protein Atu5090 [imported] - Agrobacterium tumefaciens (strain CS

RESULT 12

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Cjacession: AG3170
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I karge, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:09X2P5, GB:AE001820, GB:AE000512; NID:g4982411; PIDN:AAD368
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA'
A;Residues: 1-67 «KUR"
A;Cross-references: UNIPROT:08UKL1; GB:AE008687; PIDN:AAL45781.1; PID:g17743516; GSPDB:
A;Experimental source: strain C58 (Dupont)
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C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11.5un-1999 #sequence_revision 11.5un-1999 #text_change 09.5ul-2004
C;Accession: H72205
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: H75603
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                              ster, E.W.
A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A, Reference number: AB2577; MUID:21608550; FMID:11743193
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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59;
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Cincession to the control of the con
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A; Residues: 1-458 <WHI>
A; Cross-references: UNIPROT: Q9RZ60; GB: AB001862; GB: AB001825; NID: g6460468; PIDN: AAF1224
A; Experimental source: strain R1
C; Genetics: A; Gene: DRA0094
A; Map position: 2
C; Superfamily: Haemophilus influenzae hypothetical protein H11500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crumbs protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
38.3%; Score 42.5; DB 2; Length 458;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 11; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F,352-385/Domain: EGF homology <EGX1>
F,392-424/Domain: EGF homology <EGF1>
F,691-722/Domain: EGF homology <EGF>
F,767-799/Domain: EGF homology <EGG3>
F,1879-1914/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: FlyBase.crb
A,Cross-references: FlyBase:FBgn0000368
C,Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAMEREWAMFL-RAASSRIRGG 21
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A;Accession: H75603
A;Status: preliminary
A;Molecule type: DNA
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Search completed: November 10, 2004, 14:52:19 Job time : 6.39623 secs

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=NRC-1 / ArCC 700922 / JCM 11081;

MEDLINE=20504648; PubMed=1101690;

A MEDLINE=20504648; PubMed=1101690;

AN MUV., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

AN MELLINE S., Weir, D., Haliga N.S., Thorsson V., Sbrogna J.,

BANATZell S., Weir D., Hall J., DanNon W.J., Hough D.W.,

A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

A Leithauser T.A., Peck R.F., Pohlschroder M., Spudich J.W.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Rebardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

T. "Genome sequence of Halobacterium species NRC-1.";

BEBL; AR04988; AAG18847.1; -.

BIR, C84185, C84185.

InterPro; IPR01060; RibP_bind_barrel.

P. Fam, PF02006; DUF137; 1.

PRESF; PIRSFO04833; DUF137; 1.
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                 06291 oryza sativ
Bad07736 oryza sat
028484 archaeoglob
089924 bradyrhizob
0819k5 homo sapien
CG1jk5 photobacter
CG2255 photobacter
CG2255 photobacter
081649 homo sapien
09bia3 caenorhabdi
Q7xx14 oryza sativ
Q8mff canis famil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                           OrderedLocusNames=VNGO250.3, VNGO250C;
Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea, Buryarchaeota; Halobacteria; Halobacteriaceae; Halobacteriaceae; Halobacteriaceae; Halobacteriaceae; Malobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 2;
Pred. No. 34;
2; Mismatches
                                                                                                                                                                ALIGNMENTS
Q7XCS3
Q94HY3
Q62GHT
Q62GHT
DP2S ARCFU
Q89P24
Q61WK5
C6LJK5
CAG2252S
                                                                                                                                                                                                                                         Created)
                                                                                                  Q9BIA3
Q7XRI4
Q8MJF3
Q7YQK5
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Q7DM12;
05-UUL-2004 (TrEMBLrel. 27, C:
05-UUL-2004 (TrEMBLrel. 27, Li
05-UUL-2004 (TrEMBLrel. 27, Li
Abrin A-chain (Fragment).
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ilarity 63.2%;
Conservative
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Best Local Similarity
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SEQUENCE 249 AA;
                   Vng0250c.
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096235 abrus preca
096237 abrus preca
036237 abrus preca
038761 abrus preca
038761 abrus preca
088915 pseudomonas
081403 abrus preca
080403 streptomyce
080403 bacallus ha
07d052 agrobacteri
068095 yersania ps
062566 oryza sativ
Bad09297 oryza sativ
Bad1769 oryza sativ
Bad1769 oryza sativ
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Q8hh6 vibrio para
Q7ywb4 drosophila
Q9w7j4 drosophila
Q8m1c9 drosophila
Q8m1c9 drosophila
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084nh6 manihot esc
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sphingomona
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                                                                     November 10, 2004, 13:38:57; Search time 29.3057 Seconds (without alignments) 431.938 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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07nnr6
07x214
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     1825181 seqs, 575374646 residues
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Q83U65
Q9KD28
Q7D052
Q8UGM2
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Maximum Match 100%
Listing first 45 summaries
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111
1 GAMEREWAMFLRAASSRIRGGV 22
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BAD17669
BAD17797
Q84NH7
Q84NH6
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Q7NNR6
Q7X2L4
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Q87HU6
Q7YWB4
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Perfect score:
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46
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251 AA;
                           Query Match
Best Local Similarity
Matches 8; Conserv
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Q96237
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                                                                                                                                                                                                           Chin-Hung H., Lee M.C., Chen J.K., Lin J.Y.;

"Cloning and expression of three abrin A-chains and their mutants
derived by site-specific of three abrin A-chains and their mutants
Bur. J. Blochem. 219:83-87 (1994).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 268 FRNA.

-! SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL, X76720, CAA54138.1, -.

Interbro; IPRO01574; RIP.

Pfam; PF00161; RIP; 1

PROSITS; P800956; SHIGARICIN.

PROSITS; P8009755; SHIGARICIN.

PROSITS; P8001875; SHIGARICIN.

PROSITS; P8001875; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94139756; PubMed=8307038;
Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
Cloning and expression of three abrin A-chains and their mutants
"Cloning and expression of three abrin A-chains and coli.";
derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Blochem. 219:83-87(1994).
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01-FBB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin A chain B164A/R167L; (Fragment).
Name=pcDNAC-1-E164A/R167L;
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicotyledons; core endicots; rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Abrus precatorius (Indian licorice) (Crab's eye).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; X76644; CAA54092.1;
HSSP; P11140; IABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOS-7; FILTUS, ADM. P. Phydrolase activity, IEA. GOS-0016787; Fihydrolase activity, IEA. GO; GO:0016787; Fihydrolase activity; IEA. GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPRO1574; RIP. P. Petam; PF00161; RIP; 1.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.4%; Score 46; DB 2; Length 251; 36.4%; Pred. No. 34; tive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27997 MW; 3B60351839AEFB7E CRC64;
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                                                                                                                                                                                          MEDLINE=94139756; PubMed=8307038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 36.4 tes 8; Conservative
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                                                                                               NCBI_TaxID=3816;
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Matches
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            SO CCC CCC RATA A DRA B 
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01-FBB-1997 (TrEMBLrel. 02, Created)
01-FBB-1997 (TrEMBLrel. 02, Last sequence update)
01-OTP-2003 (TrEMBLrel. 25, Last annotation update)
PcDNAAc-1-E164A/R167L protein (Fragment).
Names-pcDNAAc-1-E164A/R167L
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spernatophyta; Wagnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
[1]
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Abrus precatorius (Indian licorice) (Crab's eye).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016787; F.hydrolase activity; IEA.
GO; GO:0030598; F.rRNA N-glycosylase activity; IEA.
GO; GO:001748; P.negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P.pathogenesis; IEA.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
11.4%; Score 46; DB 2; Length 251; ilarity 36.4%; Pred. No. 34; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
41.4%; Score 46; DB 2; Length 251;
Best Local Similarity 36.4%; Pred. No. 34;
Matches 8; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
28040 MW; D57FCB182E0EECC9 CRC64;
                                                                                                                                                                                                                                                                                    Q96236;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin A chain (E164A) (Fragment).
                                                                                                                                                                                                                                                              251 AA.
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                                                                                                                                                                                                                                                              PRT;
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                                                                                                 1 GAMEREWAMFLRAASSRIRGGV 22
                                                                                                                               11 GATSOSYKOFIEALRERLRGGL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAMEREWAMFLRAASSRIRGGV 22
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Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2243366) PubMed=12534463;
MEDLINE=2243360; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madugu K., Melson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                            Ricin A-Chain type 73 (Fragment).

Abrus precatorius (Indian licorice) (Crab's eye).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific adenosine on the 288 rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; X54973; CA4738655.1; -.
HSSP; P1140; IABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPRO01574; RIP.
Pfam; PF00161; RIP; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AA; 28229 MW; 187B8B4E134AECE5 CRC64;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                              252 AA
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                                                                                                                                                 PRT;
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12 GATSQSYKQFIEALRERLRGGL 33
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OrderedLocusNames=PP3706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3816;
                                                                                                                                                                                 038761; 096234
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01-JUN-2003
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SEQUENCE
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                                                                                Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
"Cloning and expression of three abrin A-chains and their mutants derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Biochem. 219:83-87/11294).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL: SIMILARITY: Belongs to the ribosome-inactivating protein family.
HSSP; P11140; IABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S TRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; X54812; CAA38654.1; -.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abrese; Abrus.
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GO, GO:0030598; F:RRNA N-glycosylase activity; IEA.

GO; GO:0017148; P:regulation of protein biosynthesis; IEA.

InterPro; IPR001574; RIP.

InterPro; IPR001574; RIP.

PRIM: PR001575; SHIGARICIN.

PROSITE; PS00275; SHIGARICIN.

Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                      GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030598.-F:rRNA N-glycosylase activity; IEA.
GO; GO:00105405; P:negative regulation of protein biosynthesis;
GO; GO:0009405; P:negative regulation of protein biosynthesis;
InterPro; IPR001574; RIP.
PFIMI; PR00157; RIP.
Hydrolase; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%; Score 46; DB 2; 36.4%; Pred. No. 34;
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5; Mismatches
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Pred. No. 3
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                                                      MEDLINE=94139756; PubMed=8307038;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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                             TISSUE=Seed
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SEQUENCE
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Q38760;
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RESULT 6 038760

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"Complete genome sequence and comparative analysis of the

Best Loca Matches

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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.
Davis R.W., Ecker J.R., Theologis A.;
Submitted (Apr.2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY095418; AAM20059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopšis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                          Complete proteome; Hypothetical protein.
SEQUENCE 319 AA; 35856 MW; ACA25B56E8D47F39 CRC64;
metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
02-WDL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein At2g46200.
                                                                                                                                                                                                               41.4%; Score 46; DB
llarity 44.4%; Pred. No. 43;
Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                             3 MEREWAMFLRAASSRIRG 20
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                             Environ. Microbiol. 4:799-808(;
EMBL; AE016788; AAN69303.1; -.
TIGR; PP3706; -.
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Matches 9, Conservative
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SEQUENCE 382 AA; 4
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Matches 8; Conserv
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99 Proceidates) Abrin-a B chain;

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Q83U65 C
01-JUN-2003 (TrEMBLrel. 24, La
01-JUN-2003 (TrEMBLrel. 24, La
05-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein (Unbl.)
Name=unbl.)
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Best Local Similarity
Matches 8; Conserv
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### PRINTS, PROUSSE, SHICARICIN.
### PROSETTS, PROUSSE, SHICARICIN.
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Gaps .. 0 Streptomyces carzinostaticus subsp. neocarzinostaticus. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=167636; Length 528; Created)
Last sequence update)
Last annotation update) 41.4%; Score 46; DB 1; ilarity 36.4%; Pred. No. 71; Conservative 5; Mismatches 328 AA

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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Hounnel K., Gordon J., Vaudin M., Iartchouk O., Epp. A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.",
                          Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
   Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                     MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:2323-2328(2001).
EMBL, AE008032; AAK86824.1; ...
InterPro, IPR005000; HpcH Hpal.
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Best Local Similarity
                                                                                     NCBI_TaxID=176299;
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QBUGM2
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                                                                                                                                                                                                                                            Zazopoulos E., Huang K., Staffa A., Liu W., Bachmann B.O., Nonaka K., Ahlert J., Thorson J.S., Shen B., Farnet C.M.;
"A genomics-guided approach for discovering and expressing cryptic metabolic pathways.";
Nat. Bictechnol. 21.187-190(2003).
EMBL, AY117439; AAM78015.1; -.
EMBL, AF$46157; AAO25901.1; -.
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EMBL; APOOIS11; BABOS110.1; ---
PIR; G83823; G83823.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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Liu W., Nonaka K., Nie L., Bae J., Zazopoulos E., Farnet C.M., Shen B.,
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                                                                                            Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 328 AA; 35711 MW; 7C096FF3C4BA297E CRC64;
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SEQUENCE 231 AA; 27050 MW; F30860E6ACF83ECC CRC64;
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05-UIL-2004 (T-EMBLrel. 27, Created)
05-UIL-2004 (T-EMBLrel. 27, Last sequence update)
05-UIL-2004 (T-EMBLrel. 27, Last annotation update)
AGR_C_1872p.
OrderedLocusNames=AGR_C_1872;
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Last annotation update)
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229 GATEQELALFARQAGEHRWALAQGAAFAAEARVRAGL 265
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Best Local Similarity 32.4%;
Matches 12; Conservative
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01-0CT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
BH1391 protein.
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NCBI_TaxID=86665;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 15944;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon D.,
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIATRE-216 (0856); PubMed=11743193; MEDIATRE-216 (0856); PubMed=11743193; MEDIATRE-216 (0856); PubMed=11743193; Mood D.W., Setubal J.C., Kaul R., Mood G.E., Almeida N.F. Jr., Hoo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Hoo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Datherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
                                                                             / Match
Local Similarity 52.4%; Pred. No. 53;
les 11; Conservative 3; Mismatches 7; Indels
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Pfam; PF03328; HpcH Hpal; 1.
SEQUENCE 266 AA; 27934 MW; D37F0891D97D1599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D37F0891D97D1599 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                        266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:2317-2323(2001).
EMBL, AE009066; AAL42028.1; -.
PIR; AR2701.
PIR; AR2701.
HSSP, P23522; IDXE.
GO; GO:0016228; Faldolase activity; IEA.
Interpro, IPR050500; HpcH_HpaI.
Pfam; PF03328; HpcH_HpaI.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                       236 GADVTEFANTLRALSARYKGG 256
                                                                                                                                                                                                             1 GAMEREWAMFLRAASSRIRGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27934 MW;
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us-10-092-750-50.rup

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                                                                                                                  QGEVPS;

QGEVPS;

QLOCT-2004 (TEMBLrel. 28, Created)

O1-OCT-2004 (TEMBLrel. 28, Last sequence update)

O1-OCT-2004 (TEMBLrel. 28, Last annotation update)

Putative membrane-bound sugar-binding protein.

Name=yapi89;

Yersinia pseudotuberculosis.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaies;

Enterobacteriaceae; Yersinia.
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40.5%; Score 45; DB 2; Length 1423;
Best Local Similarity 36.4%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                            7; Indels
                                                                                                         PRT; 1423 AA.
11; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         1 GAMEREWAMFLRAASSRIRGGV 22
                                     236 GADVTEFANTLRALSARYKGG 256
                     1 GAMEREWAMFLRAASSRIRGG 21
                                                                                                           PRELIMINARY;
                                                                                                         QGEVP5
Matches
                                                                                 RESULT 15
QGEVPS
ID QGEVP
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Sequence 5300, Ap Sequence 20982, A Sequence 3124, Ap Sequence 26751, A Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl Sequence 2150, A Sequence 2965, Ap Sequence 2965, Ap Sequence 20, Appl Sequence 20, Appl Sequence 31786, A Sequence 20, Appl Sequence 31786, A Sequence 20, Appl Sequence 3139, A Sequence 50, Appl Sequence 50, Appl Sequence 5139, A Sequence 5150, Appl Sequence 5
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14100, A
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                                                                                                            November 10, 2004, 13:44:14; Search time 6.58868 Seconds (without alignments) 181.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 14100
Sequence 19, 3
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

? /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

? /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

?: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-7134-20982

US-09-134-001C-1344

US-09-134-001C-1344

US-09-134-001C-1344

US-09-134-001C-1344

US-09-18-112-75

US-08-818-111-75

US-09-072-59-75

US-09-072-59-75

US-09-252-991A-21750

US-09-252-991A-21788

US-09-252-991A-31788

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989

US-09-252-991A-16989
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                                                                                                                                                                                                                                                                                                                                          478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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102
1 RGLWVDRVLEEWGLEPRQ 18
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Maximum DB seq length: 200000000
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Match Length
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Generoce 5300, Application US/09583110

Sequence 5300, Application US/09583110

Sequence 5300, Application US/09583110

Sequence 5300, Application US/09583110

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcurration of Invention: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcurrations of Price Particle Data 1000-05-26

CURRENT FILING DATE: 1000-05-26

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 5300

LENGTH: 277

MUNICH: 277
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US-09-252-991A-20982
US-09-252-991A-20982
Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINGA AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINGA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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        4956, A
27210, A
2, Appli
43, A
     Sequence 12915, A Sequence 27510, A Sequence 2710, A Sequence 2763, Applia Sequence 170, Applia Sequence 6, Applia Sequence 28, Applia Sequence 28, Applia Sequence 2, Applia Sequence 27, Applia Sequence 2800, Applia Sequence 2540, Applia Sequence 2540, Applia Sequence 5540, Applia Sequence 554
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US-09-489-039A-12915
US-09-328-322-4956
US-09-252-991A-27210
US-10-106-275-2
US-08-489-039A-8763
US-08-804-227C-15
US-08-804-227C-16
US-08-804-1298-6
US-09-118-6
US-09-118-6
US-09-118-6
US-09-118-6
US-09-118-6
US-09-118-6
US-09-118-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Streptococcus pneumoniae US-09-583-110-5300
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Cannons-Neto, Antonio
APPLICANT: Cannons-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Centor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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Pred. No. 47;
4; Mismatches 2; Indels
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ZUDY: 98104-7092
ZUDY: 98104-7092
ZUDY: 1082
ZUDY: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-818-112-75
; Sequence 75, Application US/08818112
; Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
: | | :: | : | | : | | 1: | | 1: | 170 LDRFIDEYGLNPQQ 183
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VS-09-10-279-1434

VS-09-10-279-1434

VS-09-10-279-1434

VS-09-10-279-1434

VS-09-10-279-1439

VS-09-10-279-1439

VS-09-10-279-1439

VS-09-10-279-1439

VS-09-10-279

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT PILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 4472

SOGTWARE: Parentin Ver. 2.1

SEQ ID NO 1434

LENGTH: 292
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44.1%; Score 45; DB 4; Length 292;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 5; Mismatches 2; Indels
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50.0%; Pred. No. 31;
ive 5; Mismatches 2; Indels
                                                                                                                           DB 4; Length 245;
8.6;
                                                                                                                                                                           3; Indels
                                                                                                                           Score 48; DB Pred. No. 8.6; 3; Mismatches
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                        ; TYPE: PRT
; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-20982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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165 LDRFIDEYGLNPQQ 178
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50 DRAASEWGLQPQE 62
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Best Local Similarity 50.05
Matches 7; Conservative
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  LENGTH: 245
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TREAT

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PATEUR NO. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Steky, Yasir A.W.
APPLICANT: STEWNENTION DAVIN C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                STATE: MEANINGTON

ZIP: 98104-7092

ZIP: 98104-7092

COUNTRY: USA

SIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUW TYPE: FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998

CLASSIFICATION:
ATTOMNEY/AGENT INPORMATION:
NAME: MAKY, DAVIG J.
REGISTRATION NUMBER: 31,392
REBERENCE/POCKET NUMBER: 31,392
REBERENCE/POCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

INPORMATION FOR SEQ ID NO: 75:
SEQUENCE CHRARACTERISTICS:
LENGTH: 580 cmino acids

LENGTH: 580 cmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

44.1%; Score 45; DB 3;
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches
75, Application US/09056556
3, 6350456
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                                                                                                                                                                                                                                                                                                     Washington
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STRANDEDNESS: siz
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US-09-056-556-75
                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-072-596-76
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                                                                                                                                                                                                                                                         Gaps
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Weto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF ADDRESSEE: SEED and BERRY LLP
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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44.1%; Score 45; DB 3; Length 580;
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                  Query Match
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
CONTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-691
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 76, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     1 RGLWVDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                               82 RTLGVRRTLSOWNLSPR 98
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; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 KTLGVRKTLSQWNLSPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
linear
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Gaps

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Length 580 7; Indels

single

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TUBERCULOSIS
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Patent No. 6488366

Patent No. 6488366

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Varo, Attonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomes S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel 
82 RILGVRRILSOWNLSPR 98
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
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RESULT 8 US-09-056-556-75

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Gaps

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Score 45; DB 4; Length 580;
Pred. No. 65;
1; Mismatches 7; Indels
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US-09-489-039A-7634
US-09-489-039A-7634
; Sequence 7634, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae US-09-489-039A-7634
                                                                                                                                                                                                                                                     1 RGLWVDRVLEEWGLEPR 17
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                                                                                                                                                     Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                             82 krigvrkrisownisek
          LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 50.0
Matches 7; Conservative
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TOPOLOGY:
US-09-072-967-75
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TYPE: PRT
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
44.1%; Score 45; DB 4; Length 580;
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 7; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVId J.
REGISTRATION NUMBER: 210121.417C9
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 76: SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STRTE: 8300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: Exabable FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCHEMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patertin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGLWVDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , TOPOLOGY: linear
US-09-072-596-76
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US-09-072-967-75
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NS-09-252-991A-21750

NS-09-252-991A-21750

Sequence 21750, Application US/09252991A

Patent No. 6551795

GENERAL IMPORMATION:

APPLICANT: Marc J. Rubenfield et al.

TILLS OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TILLS OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TILLS OF INVENTION: 107196.136

CURRENT PLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR SILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PRILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7634
LENGTH: 398
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43.1%; Score 44; DB 4; Length 398;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 4; Length 371; Pred. No. 57;
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42.2%; Score 43; DB 4; Length 521; 50.0%; Pred. No. 1.2e+02; tive 2; Mismatches 5; Indels
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; PRIOR FILING DATE: 1999-04-09; NUMBER OF SEQ ID NOS: 8344; SEQ ID NO 5969; LENGTH: 521; TYPE: PRT; ORGANISM: Proteus mirabilis US-09-543-681A-5969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGLWVDRVLEEWGL 14
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Matches 7; Conserv
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                                                                                                                                                 Sequence 2905, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
LENGTH: 544
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Patent No. 6605709
GRNERAL INFORMATION:
APPLICANT: GRAY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR APPLICATION NUMBER: US 60/128,706
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43.1%; Score 44; DB 4; Length 544;
Best Local Similarity 26.1%; Pred. No. 86;
Matches 6; Conservative 8; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NECOLITY
NECOLITY
Sequence 14, Application US/08840767B
Fatent No. 62574
Fatent No. 62774
Fatent Patent No. 62774
Fatent Reprization No. 62774
Fatent Reprisation No. 62774
Fatent Reprisatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 GIWGEKIMQAWNQFPAGKWGVEP 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: M.catarrhalis
US-09-540-236-2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: C. elegans US-08-840-767-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-681A-5969
                                                                             RESULT 13
US-09-540-236-2905
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Sequence 77243, A Sequence 183, App Sequence 183, App Sequence 16, App Sequence 76, App Sequence 50840, App Sequence 248057, Sequence 228961, Sequence 228961, Sequence 228961, Sequence 227309, Sequence 226, App Sequence 236, App Sequence 22659, Sequence 22659, Sequence 22639, App Sequence 22659, App Sequence 22639, App Sequence 2233, Ap

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB s Maximum DB s

Database :

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WENCH.

Sequence 63, Application US/10092750

Sequence 63, Application US/10092750

Bublication No. US2030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

TITLE OF INVENTATION: Polyeptides Interactive with BCL-X1

FILE REFREENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR APPLICATION NUMBER: US 60/274,526

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: IB

TYPE: PRI

TY
5 US-10-424-599-267456'
5 US-10-389-126-7453
4 US-10-369-493-1093
4 US-10-369-493-1093
4 US-10-369-493-1093
4 US-10-193-002-76
4 US-10-193-002-76
5 US-10-10-185-604-886
5 US-10-186-761-14817
5 US-10-186-761-14817
5 US-10-424-599-248057
7 US-10-424-599-28961
5 US-10-425-114-70225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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US-10-425-115-244728
US-10-426-24728, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Sequence 144728,
Sequence 104754,
Sequence 147554,
Sequence 115, App
Sequence 2330, App
Sequence 2765, Ap
Sequence 3765, Ap
Sequence 3765, Ap
Sequence 130, App
Sequence 130, App
Sequence 130, App
Sequence 3256, Ap
                                                                                                                                                                     November 11, 2004, 01:28:30; Search time 20.8189 Seconds (without alignments) 305.399 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 US-10-092-750-63

4 US-10-425-115-244728

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6 US-10-437-963-147554

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6 US-10-094-749-233

4 US-10-094-749-233

4 US-10-094-749-235

5 US-10-108-260A-3255

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Gapop 10.0 , Gapext 0.5
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Darbazuk, Brad Mith, Brantson: Rice Nucleic Acid Molecules and Other Molecules Associated With, TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement, FILE REFERENCE: 38-21(5321)B GURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-06-14; NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENGTH: 582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34655, Application US/10767701

Publication No. US20040172664A1

Publication No. US20040172664A1

REBERRAT: REPREMENCE:
APPLICANT: Kovalic, David K.
APPLICANT: Abou, Yihua

APPLICANT: Covalic, David K.
APPLICANT: Covalic, David K.
APPLICANT: Covalic, David K.
APPLICANT: Applicant Covalic, David K.
APPLICANT: Covalic, David K.
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 34655

LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0%; Score 51; DB 16; Length 582; Best Local Similarity 53.3%; Pred. No. 63; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C51561_1.pep
US-10-767-701-34655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: INFORMATION: Clone ID: PAT_MRT4530_48433C.1.pep
US-10-437-963-147954
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NAME/KEY: unsure
NAME/KEY: unsure
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 WFDRMITEFGIEPTE 134
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ORGANISM: Sorghum bicolor
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ORGANISM: Oryza sativa
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us-10-(
APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
ITILE OF INVENTION: Wolesic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 244728
HANGEL 198
TYPE: LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 17; Length 198;
Pred. No. 16;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: NRT4577_154781C.1.pep US-10-425-115-244728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(198)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-12429

US-10-11429

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OWURA, SATOSH

APPLICANT: ISHIKAWA, UUN

APPLICANT: ISHIKAWA, UUN

APPLICANT: ISHIKAWA, UUN

APPLICANT: SHIKAWA, UNN

APPLICANT: SHIRAWA, UNN

APPLICANT: SHIRAWA, UNN

APPLICANT: SHIRAWA, UNN

APPLICANT: HATTORI, WOSHITWI

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR PLOR FILING DATE: 2001-05-30

PRIOR PRIOR PRIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: : |:||||: ||
662 GVALFRLLEEWGVRPR 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GLWYDRYLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WVDRVLEEWGLEPRO 18
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76 WFDRMIKEFGIEPAE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
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NAME/KEY: unsure
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US-10-156-761-10429
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APPLICANT: La Rosa, Thomas J.

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Sequence 9676, Application US/10369493
; Sequence 9676, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Gao, Yongwei
    APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APLEAR APPLICANT: ON NUMBER: US/03-02-28
    APPLICANT: Goldman, Barry S.
    APPLICANT: FILMS BARRY S.
    APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 94;
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44.6%; Score 45.5; DB 9;
Best Local Similarity 69.2%; Pred. No. 63;
Matches 9; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCATION: (1). (306)
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-9676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PARCENTIN VET: 3.0
SOFTWARE: PARCENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5765, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHT, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| :||| :|||
180 RGLWDYIDRVRQEYG 194
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T: OCHIAI, KEIKO
T: YOKOI, HARUHIKO
T: TATEISHI, NAOKO
T: SENOH, AKIHIRO
T: IKEDA, MASATO
T: OZAKI, AKIO
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Best Local Similarity 54.5%; Pred. No. 59;
Matches 12; Conservative 2; Mismatches 4; Indels
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Best Local Similarity 46.7%; Pred. No. 49;
Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAGAL, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: OSHIKAWA, TSUTOMU
APPLICANT: OSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENUT
APPLICANT: NAGHARI, KENUT
APPLICANT: NAGHARI, KENUT
APPLICANT: NAGHARI, KENUT
APPLICANT: NAGHARI
APP
FILE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 115
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2330, Application US/10094749
Publication No. US20030219741A1
GENERAL INPORMATION:
APPLICANT: ISOGAI, TRKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TESUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
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PRIOR APPLICATION NUMBER: 60/550,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PRICENTIN VOY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 WVDRVLEEWGLEPRO 18
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54 WVPRLLQEWKPRPQE 68
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OTSUKA, KAORU
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US-10-094-749-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-769-787-115
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US-10-424-599-148079

US-10-424-599-148079

Sequence 148079, Application US/10424599

Publication No. US20040031072A1

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 148079

LENGTH: 49
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APPLICANT: A Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 267456
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                                                                                                                                                                                                                                                                               Length 177;
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Best Local Similarity 47.4%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                         Indels
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US-10-424-599-148079
                                                                                                                                                                                                                                                                        Query Match
44.6%; Score 45.5; DB 15;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(49)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 267456, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GLWVDR----VLEEWGLEP 16
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGLWVDR-VLE--EWG 13
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3256
LENGTH: 177
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ORGANISM: Glycine max
FEATURE:
NAME/KEY:
LOCATION: (1)..(49)
                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Glycine max FEATURE:
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US-10-424-599-267456
                                                                                                                                                                                                                        US-10-108-260A-3256
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                                                                                                                                                                                                                            RESULT 10
US-10-100-260A-3255
; Sequence 3255, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
    APPLICANT: HELLY RESEARCH INSTITUTE
; TILLE OF INVENTION: No. US20040005560A1e1 full length cDNA
    TILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT PILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Petentin Ver. 2.1
; SEQ ID NO 3255
; LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Jack Annual Control of State o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-108-260A-3256
US-10-108-260A-3256
Sequence 3256, Application US/10108260A
Sequence 3256, Application No. US20040005560A1
GENERAL INFORMATION
TITLE OF INVENTION: No. US20040005560A1e1 full length CDNA
TITLE OF INVENTION: No. US20040005560A1e1 full length CDNA
CURRENT APPLICATION WHORER: US/10/108,260A
CURRENT PILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
44.6%; Score 45.5; DB 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGLWVDR-VLE--EWG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 RGLWVIRKVLEESEWG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WVDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 WSDRV---WGAEPR 18
                                                                                           || |:|:|| |||
75 VDTVIEQWG-EPR 86
                                                              5 VDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-108-260A-3255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-002-631C-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-002-631C-130
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Gaps

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APPLICANT: Carr, Grand
APPLICANT: Amamonco, Robert
APPLICANT: Forsyth,
TILLE APPLICANT: Xu,'H.
TILLE NETRENCE: ELITRA.034A
TILLE REFERENCE: ELITRA.034A
CURRENT PAPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-24
PRIOR PELING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2001-02-09
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   2;
                                                                                                               Score 45; DB 15; Length 131;
Pred. No. 1e+02;
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Pred. No. 2.3e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                               4; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83536C.1.pep
US-10-424-599-267456
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 77243, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 RNLWLPAGVEPVWKDWGLSP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGLW----VDRVLEEWGLEP 16
                                                                                                           Query Match
Best Local Similarity 47.1%; Pr
Matches 8; Conservative 3;
                                                                                                                                                                                                                                                                       3 LWVD--RVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                   19 LWSDPEDIVDNWGLSPR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Framick, John
APPLICANT: Framico, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
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Search completed: November 11, 2004, 02:43:19
Job time : 21.8689 secs
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-63 102 1 RGLWVDRVLBEWGLEPRQ 18 Title: Perfect score:

Scoring table: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P-glyco	P-glycoprotein - S	hypothetical prote	phosphoesterase-re	phosphoesterase-re	hypothetical prote	_	ŭ	c	hypothetical prote	conserved hypothet	probable hexosyltr	hypothetical prote	multidrug efflux p	phosphoprotein pho	hypothetical prote	TRM23b IS ATP-bind	TRM23b IS ATP-bind	GumM protein XF236	probable permease	hypothetical prote	hypothetical prote	probable homeodoma	otein	phosphoprotein pho	hypothetical prote		CEM-1 protein - Ca	probable tartrate
	Д	T18344	T18343	G72634	B95072	H97939	S23603	B83861	T30358	T08480	T40079	D82233	F64500	B75067	AB0370	A45640	G70603	C95314	D95334	D82566	G83248	T05178	T15795	F84565	4	842559	544858	82	5501	364
	DB	5	7	7	Н	Н	7	7	~																					
	Length	1677	<b>L</b> ~	288	277	277	192	338	244	97	199	290	390	437	1043	303	97	245	245	265	310	1308	686	220	305	305	372	395	418	451
ж	당당		ö		φ,		46.6	46.1	45.1	44.1	44.1	44.1	44.1	٠	44.1	•	43.1	•	ω.	•	3	43.1	•	•	•	•	•	42.2	•	•
	Score			20	49	49	47.5	47	46	45	45	45	45	45	45	44.5	44	44	44	44	44	44	43.5	ぜ	43	43	43	43	43	43
	Result No.		7	m	4	ഗ	9	7	œ	σ	10	11	12	13														27		

hypothetical prote glucosyltransferas	56K serine protein probable selenium-	probable beta-gala helicase related p	hypothetical prote	probable MFS trans	hypothetical prote		core antigen - gro	homeodomain protei	two-component resp	histidinol-phospha	hypothetical prote
G72205 T40396	PRBEI1 D84549	T04269 AC1065	D71543	H83556	T20/97 B84152	E64087	NKVLS	H85433	AH1815	A35397	E86634
0 0	н 0	<b>(1</b> (1)	N	01	N 10	4 1	Н	~	~	~	7
473 506	518 715	729 1249	298	438	767	192	217	217	224	361	389
42.2	42.2 2.2	42.2	41.7	41.7	2.1.2	41.2	41.2	41.2	41.2	41.2	41.2
m m	4 4 9 9	43	42.5	42.5	4 2	4 4	42	42	42	42	42
ক'ক'			4	4,							

## ALIGNMENTS

RESULT 1

	T18344
	P-glycoprotein E - Leishmania tropica
	C;Species: Leishmania tropica
	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
	C; Accession: T18344
	R; Lafuente, E.; Castanys, S.; Gamarro, F.
_	submitted to the EMBL Data Library, April 1996
_	A;Reference number: Z18880
_	A; Accession: T18344
-	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
	A;Residues: 1-1677 <laf></laf>
	A.Cross-references: UNIPROT:000805; EMBL:US5381; NID:g1916605; PID:g1916606; PIDN:AABS1
	C;superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
_	Query Match 52,9%; Score 54; DB 2; Length 1677;
	Similarity 56.2%; Pred. No. 9.5;
	Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
	Oy 1 RGLWURVLEEMEP 16
	Db 45 RSLWAORVSDLWCTEP 60

Paraous 2
Peglycoprotein - Sauroleishmania tarentolae
Peglycoprotein - Sauroleishmania tarentolae
Ciptedes: Datoben. Parasitol. 68, 81-91, 1994
A; Filegare, D.; Hettema, B.; Ouellette, M.
Mol. Biochem. Parasitol. 68, 81-91, 1994
A; Filestence number: Z18879; MUID:95198776; PMID:7891750
A; Reference number: Z18879; MUID:95198776; PMID:7891750
A; Rolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1724 *LEG>
A; Residues: 1-1724 *LEG>
A; Coptedes: NID:9460312; PID:9460313; PIDN:AAA6555; C; Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match

50.0%; Score 51; DB 2; Length 1724;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 4; Indels

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Gaps

.. 0

47 LWKQRVIDLWGAEP 60 3 LWVDRVLEEWGLEP 16 g ò

RESULT

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A;Accession: H97939
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99348.1; PID:g15458120; GSPDB:GN00174
C;Comment: Although this sequence has motifs characteristic of a variety of phosphoestes C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces coelicolor
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23603
FFernandez-Morenda-Martin-Triana, A.J.; Martinez, E.; Niemi, J.; Kieser, H.M.; H
J; Bacteriol. 174, 2958-2967, 1992
A;Title: abaA, a new pleiotropic regulatory locus for antibiotic production in Streptom
A;Reference number: S23601; MUID:92234955; PMID:1569025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: S23603
A,Accession: S23603
A,Accession: S23603
A,Accession: S23603
A,Accession: S23603
A,Accession: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Accession: 1-192 <FER>
A,Cross-references: UNIPROT: Q53897; EMBL: X60316; NID: 946793; PIDN: CAA42866.1; PID: 95816
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                                                                                                                                                                                                                       A;Gene: spr0544
C;Superfamily: phosphoesterase, MJ0912 type; phosphoesterase core homology
F;4-67/Domain: phosphoesterase core homology <PEC>
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A; Reference number: A97872; MUID: 21429245; PMID: 11544234
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                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47.5; DB Pred. No. 9.3; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein A - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGLWVDRVLE----EWGLEPRQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 RGNWDDRVLEALDGQYGLEDPQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 RĠĽCIVĎALAĚĖWĠWTPR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGLW-VDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.68;
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Matches 7; Conservative
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Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Start codon: GTG
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A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A5000; MUID:21357209; PMID:11463916
A; Molecule type: DNA A; Residues: 1-277 ckUR> A; Comment: Although this sequence has motifs characteristic of a variety of phosphoester C; Genetics: Spoil B; Spoil 
                                                         Cipecides: Aeropyrum pernix
Cipecides: Aeropyrum pernix
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cipate: 20-Aug-1999 #sequence of revision 7.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; Kahama, M.; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: G72534
A; Accession: G72534
A; Assidues: 1-288 «KAW»
A; Residues: 1-288 «KAW»
A; Cross-references: UNIPROT: Q9YBRS; DDBJ: AP000061; NID:g5104821; FIDN: BAA80533.1; PID:g5
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 288
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                                     pothetical protein APE1534 - Aeropyrum pernix (strain K1)
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Query Match
Best Local Similarity 54.5%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches

1 RGLWVDRVLE----EWGLEPRQ 18 

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63

DB 2;

Score 50; DB 2 Pred. No. 6; 2; Mismatches

Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative

A; Gene: APE1534

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||| |||: || |: | 151 RGLGSDRVVAEWWLDSR 167 1 RGLWVDRVLEEWGLEPR 17

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Gaps

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probable hexosyltransferase (EC 2.4.1.-) MJ1607 - Methanococcus jannaschii probable hexosyltransferase (EC 2.4.1.-) MJ1607 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: F64500 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, D.; Fleischmann, R.D.; Sutton, G.G.; Blake, rsoi, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Authors: Kaine, B.D.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogonic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUD:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-390 <BUL>
A;Cross-references: UNIPROT:Q59002; GB:U67601; GB:L77117; NID:g2826439; PIDN:AAB99629.1
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44.1%; Score 45; DB 1; Length 390;
Best Local Similarity 37.5%; Pred. No. 45;
Matches 9; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 290;
                                                        Length 199;
                                                                                                                       Indels
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C,Superfamily: probable hexosyltransferase ytxN
C,Keywords: glycosyltransferase; hexosyltransferase
                                                           ..
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                                                     Score 45; DB 2
Pred. No. 23;
2; Mismatches
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Best Local Similarity 45.0%; Pred. No. 33;
Matches 9; Conservative 3; Mismatches
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C,Superfamily: hypothetical protein H11400
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                                                        44.1%;
ilarity 61.5%;
Conservative
                                                                                                                                                                                   3 LWVDRVLEEWGLE 15
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
N
A; Map position:
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C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: T08480
R; Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A; Title: Conservation of the genetic switch between replication and transfer genes of In A; Reference number: 216434; MUID:97118926; PMID:8954881
A; Accession: T08480
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: LNA
A; Molecule type: LNA
A; Molecule type: LNA
A; Costeriors: EmbL:U67194; NID:g1572520; PIDN:AAC64424.1; PID:g1572529
                                                                                                                    hypothetical protein SPBC29A3.08 - fission yeast (Schizosaccharomyces pombe)
(Species: Schizosaccharomyces pombe
(Species: Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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Pred. No. 20;
6; Mismatches
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RGLYGDALIEALGLKPKE 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative 6
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: mRNA
A;Mosecule type: mRNA
A;Residues: 1-303 < ERO.
A;Cross-references: UNIPROT: Q27787; GB:M74168; NID:g162210; PIDN:AAA73084.1; PID:g162212
A;Experimental source: subsp. rhodesiense
A;Experimental source: subsp. rhodesiense
A;Note: sequence extracted from NGBI backbone (NCBIN:78241, NCBIP:78244)
C;Superfamily: Serine/threonine protein phosphatase; phosphasese core homology; phos C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec: F;17-276/Domain: phosphoroetin phosphatase homology < PPE>
F;17-276/Domain: phosphoroeterase core homology < PPE>
F;51,53,79/Binding site: iron (Asp, His, Asp) #status predicted
F;91,111,161,235/Binding site: iron (Asp, His, Asp) #status predicted
F;82,112,259/Active site: Asp, His, Tyr #status predicted
F;83,208/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.6%; Score 44.5; .DB 2; Length 303; 56.2%; Pred. No. 42; tive 1; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 10, 2004, 14:52:29 Job time : 5.41509 secs
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Best Local Similarity 56.23
Matches 9; Conservative
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AB0370
multidrug efflux protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Species: O2-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0370
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Genor-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Mnitchead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB00370
A;Accession: AB0370
A;Accession: AB0370
A;Residues: 1-1043 -KUR>
A;Rociule type: DNA
A;Residues: 1-1043 -KUR>
A;Coss-references: UNIPROT:Q8ZCE8; GB:AL590842; PIDN:CAC922285.1; PID:g15980996; GSPDB:GCGGnetics:
C;Genetics:
A;Gene: YPO0043
C;Superfamily: acriflavin resistance protein
                                                                                                                                                                                                                                                                                                Cipecies: Pyrococcus abyes:
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Rianonymous, Genoscope
submitted to the EMBL Data Library, July 1999
Albestription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
Albestription: Pyrococcus abyssi genome sequence: number: Afford Albestription: Pyrococcus abyssi genome sequence: Albestription: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru
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A45640
phosphototein phosphatase (EC 3.1.3.16) 2A catalytic chain - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accondu, N.E.; Donelson, J.E.
R;Erondu, N.E.; Donelson, J.E.
A;Title: Characterization of trypanosome protein phosphatase 1 and 2A catalytic subunite
A;Reference number: A45640; MUID:92131067; PMID:1663579
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                                                                                                                                                                                                                                                                hypothetical protein PAB1355 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 2; Length 437; Pred. No. 51; 2; Mismatches 3; Indels
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44.1%; Score 45; DB 2; Length 104

Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 8; Conservative 4; Mismatches 2; Indels
          328 GIWVYPKNPDSIAWGVDRVLSDWG 351
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Best Local Similarity 61.5%;
Matches 8; Conservative
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416 VERVMSEEGLDPRE 429
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WVPRVIEDISLEP 43
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                                                                                                                                                                RESULT 13
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November 10, 2004, 13:38:57; Search time 23.9774 Seconds (without alignments) 431.938 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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102
1 RGLWVDRVLEEWGLEPRQ 18
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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	Description		Q72kg3 thermus the	m		Q8zy05 pyrobaculum			O7exy6 oryza sativ		Q25425 leishmania	Q9ybr5 aeropyrum p			Q74el6 geobacter s		Q8dqq8 streptococc		Q8p0h0 streptococc					Q706m5 pseudomonas	Cae92925 pseudomon	Q6jei3 pichia memb	Aat12523 pichia me		Q6h193 pichia ferm	Q80x17 mus musculu	رب -		Q93re7 bacillus sp
SUMMARIES	Ç.	1	Q72KQ3	AAS80683	000805	Q8ZY05	Q93HI8	Q8GQ42	Q7EXY6	BAD10739	Q25425	Q9YBR5	Q7MM50	Q8D8B7	Q74EL6	AAR34273	80008	905260	Овьоно	Q99Z82	Q7CF02	Q7CN48	Q9WBJ8	Q706M5	CAE92925	Q6JEI3	AAT12523	оен188	Ф6Н193	Q80XL7	Q8BLU5	Q9UVA0	Q93RE7
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Q53897	60H090	AAS49425	Q9KC84	Q8KL87	Q8A7A2	Q6QJD3	AAS57792	Q721M4	Q6PSL5	AAS92601	Q9YMW3	Q8XSC4	Q8U4S7
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192	173	173	338	388	391	631	631	174	1151	1151	244	323	363
46.6	46.1	46.1	46.1	46.1	46.1	46.1	46.1	45.6	45.6	45.6	45.1	45.1	45.1
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## ALIGNMENTS

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627 AA

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"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=INAZ / AICC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                              Archaea, Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ACYlamino-acid-releasing enzyme, conjectural.
OrderedLocusNames=PAE1002;
                                                                                                    PRT;
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45 RSLWAORVSDLWGTEP
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Best Local Similarity 64.7.
Best Local 11; Conservative
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                                                                                                                         Q8ZYO5;
01-MAR-2002
01-MAR-2002
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NCBI_TaxID=5666;
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                         Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Goll O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
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                                                                                                                                                                                                                                                                                                                                                               53.9%; Score 55; DB 2; Length 241; 78.6%; Pred. No. 4.5; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                     Nat. Biotechnol. 22:547-553(2004).
EMBL. AE017302; AAS80683.1; -.
ATP-binding.
SEQUENCE 241 AA; 26385 MW; 549D15A22276994D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50929; ABC_TM1F; 2.
PS00211; ABC_TRANSPORTER 1; UNKNOWN_1.
PS50093; ABC_TRANSPORTER_2; 2.
PS00962; RIBÖSCMAL, S2 1; UNKNOWN_1.
PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1677 AA
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Best Local Similarity
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Leishmania tropica.
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                      Thermus.
NCBI_TaxID=262724;
                                                                                  SEQUENCE FROM N.A.
PubMed=15064768;
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                                                                                                                                                                                                                                       thermophilus."
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ATP-binding
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                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avermitilis.
Bacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomyces.
NCBI_TaxID=33903,
                                                                                                                                                        51.0%; Score 52; DB 2; Length 627; 64.7%; Pred. No. 34; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                     627 AA; 69906 MW; D115B4D625AF09DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2004 (TrEMBLrel. 28, Last annotation update)
Modular polyketide synthase.
Name=olmA4; OrderedLocusNames=SAVZ892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL, AE009798; AAL63191.1; --
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR0010979; Ser estrs.
InterPro; IPR011042; Tolb_C.
                                                                                                                                                                                                                                                                                                                                                                                PRT; 3970 AA
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WEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948;
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1 RGLWVDRVLEEWGLEP 16

à

512 AA

PRT;

||| ||||:: 46 DRVATEWGLQPQE 58

21:526-531 (2003).

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Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Barnattophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 51; DB 2; Length 512; Best Local Similarity 53.3%; Pred. No. 39; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A. SACQUENCE FROM N.A. SASSANT T., Matsumoto T., Katayose Y.; Sassaki T., Matsumoto T., Katayose Y.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; A500649; BAD10739.1; ... InterPro; IFR0002865; PPR. InterPro; IFR008940; Prenyl_trans. InterPro; IFR008940; Prenyl_trans. InterPro; IFR00956; PPR; 7. TIGRENOF6; PPR; 5. TANTH E
                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                             Selenium binding protein-like protein.
Name=OSJNBa0016N23.128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 GRWVHATLRRWGVEP 191
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                                                                                                                   PRELIMINARY;
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Q7EXY6
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                                                              DR GO: 00040024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.

GO: 00:00040024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.

BR GO: GO:00040360; F:NADPH:quinone reductase activity; IEA.

GO: GO:0004070; F:transferzes activity; IEA.

BR GO: GO:0006370; F:transferzes activity; IEA.

BR GO: 00:0008120; F:transferzes activity; IEA.

BR GO: GO:0008120; F:transferzes activity; IEA.

BR GO: GO:0008120; P:fatty acid biosynthesis; IEA.

BR GO: GO:0008120; P:fatty acid biosynthesis; IEA.

BR InterPro: IPR002027; Ac_transferze.

BR InterPro: IPR002027; Ac_transferze.

BR InterPro: IPR00109; Man.

BR InterPro: IPR00109; Ketoacyl synth.

BR InterPro: IPR001094; Ketoacyl synth.

BR InterPro: IPR001094; Ketoacyl synth.

BR InterPro: IPR00109; Act act acrystal.

BR Ffam; PF00100; ADH_Zinc_N; 1.

BR Pfam; PF00100; Act act acystal.

BR Pfam; PF00100; ADH_Zinc_N; 1.

BR PROSITE; PS00102; ACP DOMAIN; 2.

BR PROSITE; PS00102; ACP DOMAIN; 2.

BR PROSITE; PS00102; ACP DOMAIN; 2.

BR PROSITE; PS010162; ACP DOMAIN; 1.

BR PROSITE; PS010162; ACP DOMAIN; 1.

BR PROSITE; PS01062; BETOACYL SYNTHASE; 1.

BR PROSITE; PS01012; ACP DOMAIN; 2.

BR PROSITE; PS010162; ACP DOMAIN; 2.

BR PROSITE; PS010162; ACP DOMAIN; 1.

BR PROSITE; PS010162; ACP DOMAIN; 2.

BR PROSITE; PS010162; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; ACP DOMAIN; 3.

BR PROSITE; PS010162; ACP DOMAIN; ACP DOMAIN; 4.12662 MM; A93ESB3FAFAGBC47 CRC64;
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Merkl R., Wiehlmann L., Fritz H.J., Tummler B.;
"Gene islands integrated into tRNA(Gly) genes confer genome diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.0%; Score 52; DB 2; Length 3970; 56.2%; Pred. No. 2.2e+02; ive 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on a Pseudomonas aeruginosa clone.";
J. Bacteriol. 184:6665-6680(2002).
EMBL. AF440523; AAN62162.1; -.
SEQUENCE 245 AA, 27314 MW; 86DA12B9069ACA7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEWBLrel. 23, Created)
01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
Hyporhetical protein ORF C68.
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MEDLINE=22313472; PubMed=12426355;
Nat. Biotechnol. 21:526-531(200
EMBL; AB070340; BAB69199.1; -.
EMBL; AP065032; BAC70603.1; -.
HSSP; P25715; IMLA
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q8GQ42;
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OLYMR-2004 (TERMELrel. 27, Created)
02-MAR-2004 (TERMELrel. 27, Last sequence update)
07-MAR-2004 (TERMELrel. 27, Last sequence update)
05-MAR-2012 (TEMELrel. 27, Last sequence update)
05-MAR-2012 (TEMELrel. 27, Last sequence update)
07-YZA sativa (Japonica cultivar-group)
07-YZA STERPLOPHYTE, EMDYOPHYTE; EMDYOPHYTE; EMDYOPHYTE; EMLANTOLIGES; Poaceae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; ÷ BAC 50.0%; Score 51; DB 2; Length 512; 53.3%; Pred. No. 39; ive 1; Mismatches 6; Indels STRAIN=cv. Nipponbare;
Sasaki T., Matsunco T., Katayose Y.;
Sasaki T., Matsunco T., Katayose Y.;
Subrated activa nipponbare(GA3) genomic DNA, chromosome 8, 10ne:OSJNBa0016N23:";
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006049; BAD10739:1; 7813DC1C3B5FB4D6 CRC64; 512 AA PRT; RESULT 9 Q25425

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6 DRVLEEWGLEPRQ 18

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Query Match
Best Local Similarity 58.88
Matches 10; Conservative
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=196600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen.";
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Matches
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Q7MM50
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GO; GO:0004602; P:ATP binding; IEA.
GO; GO:0004009; P:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0004009; P:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:000610; P:transport; IEA.
InterPro; IPR001527; ABC membrane 1.
InterPro; IPR001527; ABC membrane 1.
InterPro; IPR00140; ABC membrane 1.
Pfam; PF00664; ABC membrane; 2.
Pfam; PF00664; ABC membrane; 2.
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                                                                                        P-glycoprofein.
Leishmania tarentolae (Sauroleishmania tarentolae).
Leishmania tarentolae (Sauroleishmania tarentolae).
Leishmania tarentolae (Kinetoplaetida; Trypanosomatidae; Leishmania; NCBI_TaxID=5689;
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                                                                                                                                                                                                                                                                                                     Legare D., Hettema B., Ouellette M.;
"The P-glycoprotein-related gene family in Leishmania.";
Mol. Biochem. Parasitol. 68:81-91(1994).
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; L29488; AAA65541.1; -.
PIR; T18343; T18343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1724 AA; 188967 MW; A8FE6CD4A65FA195 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                           (TremBlrel. 01, Created)
(TremBlrel. 01, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APB1534.
OrderedLocusNames=APB1534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 AA.
PRT; 1724 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA; 2.
PROSITE; PS50929; ABC_TMIF; 2.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
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                                                                                                                                                                                                                                                          STRAIN=Taril;
MEDLINE=95198776; PubMed=7891750;
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NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LWVDRVLBEWGLEP 16
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
    PRELIMINARY;
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                             01-NOV-1996
01-NOV-1996
                                                                                      01-OCT-2003
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SEQUENCE
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    Q25425
Q25425;
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Q9YBR5;
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Q9YBR5
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Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Chen C.-Y., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
"Comparative genome analysis of Vibrio Vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
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EMBL, AR00534; BAC93987.1; -.

GO, GO:000367; F:DNA binding; IEA.

GO, GO:000387; F:DNA directed DNA polymerase activity; IEA.

GO, GO:0006260; P:DNA replication; IEA.

InterPro; IPRO04013; PHP_C.

InterPro; IPRO04013; PHP_C.

Pfam; PF02231; PHP_C.

Pfam; PF02231; PHP_C.

SEQUENCE 293 AA; 33152 NW; 62C1C56AF17720BC CRC64;
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Bacteria v. Protecobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=VV1223;
Vibrio vulnificus (strain YJ016).
Batteria, Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.0%; Score 50; DB 2; Length 293; 50.0%; Pred. No. 31; ive 3; Mismatches 3; Indels
                                                                                                                                     49.0%; Score 50; DB 2; Length 288; 58.8%; Pred. No. 31; tive 2; Mismatches 5; Indels
EMBL; AP000061; BAA80533.1; -.
pIR; 072634; 072634
Complete proteone; Hypothetical protein.
SEQUENCE 288 AA; 32176 MW; 40235FA12BDD6AFB CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last ambotation update)
Predicted metal-dependent phosphoesterases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
predicted metal-dependent phosphoesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AA.
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151 RGLGSDRVVAEWWLDSR 167
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Streptococcus.
NCBI_TaxID=171101;
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Q8DQQ8
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STRAINs-PCA / ATCC 51573;

STRAINs-PCA / ATCC 51573;

STRAINs-PCA / ATCC 51573;

SEGN J. A. Paulsen I.T., Nelson W.C.,

Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,

Haidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,

Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

GWINN M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,

Van Aken S.E., Lovley D.R., Braser C.M.;

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
"Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2012) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0003677; FAOA1387.1;
R GO; GO:0003677; FIDNA binding; IEA.

R GO; GO:0003687; FIDNA-directed DNA polymerase activity; IEA.

R GO; GO:0005260; FIDNA-directed DNA polymerase activity; IEA.

R INTERPO: PROMON FIDNA FEDICATION; IEA.

R INTERPO: IPR003041; PSETERASE_FHP_N.

R INTERPO: IPR004013; PHP_C.

R Pfam; PR02811; PHP_C; 1.

R Pfam; PR02811; PHP_N; 1.

R SMART; SM0481; POLITIAC; 1.

R COMPLETE PROTECTED.

OCMPLETE PROTECTED.

OCMPLETE PROTECTED.
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                                                                                                                                                                         / Match 49.0%; Score 50; DB 2; Length 293; Local Similarity 50.0%; Pred. No. 31; les 10; Conservative 3; Mismatches 3; Indels
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                     842 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 1.
SWART; SM00267; DUF1; 1.
SWART; SM00304; HAMP; 1.
SWART; SM00304; HAMP; 1.
SWART; SM00091; PAS; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                       1 RGLW----VDRVLEEWGLEP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 environments.";
Science 302:1967-1969(2003).
EMBL; AE017180; AAR34273.1; -
TIGR; GSU0946; -.
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PROSITE; PS50887; GGDEF; 1.
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                                                                                                                                                                                                                                                                                                                                                                      ORFNames=GSU0946;
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SEQUENCE FROM N.A.

STRAIN=PCA / ATCC 51573;

STRAIN=PCA / ATCC 51573;

BubMed=14671304;

Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,

Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,

Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J., Khouri H.M., Peldblyum T.V., Utterback T.R.,

Wan Aken S.E., Lovley D.R., Fraser C.M.;

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                Gaps
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geobacter sulfurreducens,
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfuromonadales;
Geobacteraceae, Geobacter.
NCBL_TaxID=35554;
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                                                                                                                                        2; Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 2; Length 842;
Pred. No. 91;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
PROSITE; PS50885; HAMP; 1.
PROSITE; PS50113; PA6; 1.
PROSITE; PS50112; PA5; 1.
SEQUENCE 842 AA; 92860 MW; 989697FE4637E9AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             842 AA; 92860 MW; 989697FE4637E9AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR34273 PRELIMINARY; PRT; 842 AA.
AAR34273;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBDQQ8;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein spr0544.
                                                                                                                                     Score 50; DB
Pred. No. 91;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE017210; AAR34273.1; -. TIGR; GSU0946; -.
                                                                                                                                     49.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 49.0%;
Local Similarity 83.3%;
es 10; Conservative
                                                                                                                    Ouery Match
Best Local Similarity 83.3
                                                                                                                                                                                                                                                                                                   680 VDRVLEETGLDP 691
                                                                                                                                                                                                                                              5 VDRVLEEWGLEP 16
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RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robettson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y. P., Yongteck D.R., Jr., Rockey P.,
RA Gook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RY Genome of the bacterium Streptococcus pneumoniae strain R6.";
R. J. Bacteriol. 183:5709-5717(2001).
DR EMBL, AECO91831, AAK9348 1.; -.
DR PIR, H97393, H8704843, M-Pesterase M.0912.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006186; T.phtase_apaH.
DR InterPro; IPR006186; T.phtase_apaH.
DR PIRS: PIRSF000883; Pesterase M.0912.
DR Probom; PD000252; T.phtase_apaH; 1.
DR Probom; PD000252; T.phtase_apaH; 1.
SQ SEQUENCE 277 AA; 31507 MW; 7A773F94DCA187F9 CRC64;
Best Local Similarity 54.5%; Pred. No. 42; Hodels 4; Gaps 1;
Best Local Similarity 54.5%; Pred. No. 42;
Best Local Similarity 54.5%; Pred. No. 42;
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Search completed: November 10, 2004, 14:50:36 Job time : 25.9774 secs

8 8

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Sequence 5476, Ap Sequence 5123, Ap Sequence 11, Appl Sequence 11, Appl Sequence 52, Appl Sequence 16, Appl Sequence 16, Appl Sequence 15, Appl Sequence 15, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 51, Appli Sequence 61, Appli Sequence 62, Appli
                                                                                            November 10, 2004, 14:55:47; Search time 12.9537 Seconds (without alignments) 143.349 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*

(GGTZ_6/ptodata/1/iaa/5A_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/5B_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/6A_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/6B_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/PGTUS_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/PGTUS_COMB.pep:*

(GGTZ_6/ptodata/1/iaa/PGTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-543-681A-5323
US-09-1328-452A-918
US-09-1328-872A-918
US-09-1328-872A-918
US-09-1328-872A-918
US-08-469-486-52
US-08-469-486-52
US-09-252-991A-16662
US-09-252-991A-16662
US-09-252-991A-25635
US-09-252-991A-25635
US-09-252-991A-25635
US-09-252-991A-15662
US-08-924-695A-55
US-08-924-695A-55
US-08-924-695A-52
US-08-924-695A-52
US-08-924-695A-51
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                              US-10-092-750-64
157
1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28
                                                                                                                                                                                                                                                                                 478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
                Copyright
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                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                   Searched:
                                                                                                Run on:
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Sequence 43062, A Sequence 132, App Sequence 132, App Sequence 22906, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2422, A Sequence 2422, A Sequence 23079, A Sequence 23079, A Sequence 23079, A Sequence 9371, Appatent No. 5183745 Sequence 85, Appli Sequence 87, Appli Sequence 87, Appli	QUENCES RELATING TO ACINETOBACTER THERAPEUTICS	Length 614; ; Indels 0; Gaps 0;	QUENCES RELATING TO PROTEUS MIRABI
US-09-270-767-43062 US-08-961-083-132 US-09-252-991A-22906 US-08-9583-110-5075 US-08-9583-110-5075 US-09-351-550-2 US-09-351-550-2 US-09-252-991A-30608 US-09-252-991A-24228 US-09-252-991A-24228 US-09-252-991A-2428 US-09-252-991A-2428 US-09-252-991A-2428 US-09-489-039A-9371 5183745-6 US-08-785-2 US-08-924-695A-85 US-08-924-695A-85	ALIGNMENTS  109-328-5476  109-328-552-5476  109-328-552-5476  109-328-552-5476  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352  109-328-352-5476  109-328-352-5476  109-328-352-5476	ore 52; DB 4; ed. No. 9; Mismatches 8 27	09543681A CID AND AMINO ACID SEQUENCES ICS AND THERAPEUTICS S/09/543,681A 60/128,706
29.3 29.3 29.3 29.3 29.3 29.3 29.3 29.3	RESULT 1 US-09-328-352-5476 Sequence 5476, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION TITLE OF INVENTION: BUCLEIC ACID AND AMINA TITLE OF INVENTION: BUCKEIC ACID AND AMINA CURRENT APPLICATION NUMBER: US/09/328,352 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 5476 LENGTH: 614 TYPE: PRT	h Similarity 40.9%; Pr. 9; Conservative 5; 6 GWRLQNIGDDMDHAICGHDVRL	SULT 2 Sequence 5323, Application US/09543681A Patent No. 605079 BATENT S. 605079 TITLE OF INVENTION: APPLICANT: GARY BRETON TITLE OF INVENTION: FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT APPLICATION NUMBER: US/09/543,681A PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR PRIOR FILING DATE: 1999-04-09 SEQ ID NO 5323 LENGTH: 88 TYPE: PRI TYP
00000000000000000000000000000000000000	RESULT 1 US-09-328-352-5476 ; Sequence 5476, Mg; Patent No. 65629; GENERAL INFORMATI; APPLICANT: GARY ; TITLE OF INVENTY; ; TITLE OF INVENTY; ; FILE REFENCE; ; CURRENT APPLICANT; ; FILE REFENCE; ; CURRENT FILING I; ; NUMBER OF SEQ II; ; SEQ ID NO 5476 ; SEQ ID NO 5476 ; LENGTH: 614 ; TYPE: PRT  ORGANISM: Acine US-09-328-352-5476	Query Match Best Local Si Matches 9; Qy 6 G	RESULT 2 US-09-543-681A-5323 Sequence 5323 Ap Patent No. 660570 JAPANTI INFORMATI APPLICANT: GARY TITLE OF INVENTI TITLE OF INVENTI FILE REFERENCE: CURRENT APPLICATIO PRIOR APPLICATIO PRIOR PLING DAT NUMBER OF SEQ ID SEQ ID NO 5323 LENGTH: 88 TANNER PRIOR PLING DAT NUMBER OF SEQ ID SEQ ID NO 5323

. 0

Gaps

. 0

Score 50; DB 4; Length 88; Pred. No. 2; 7; Indels 1; Mismatches 7; Indels

Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative

mirabilis

TYPE: PRT; ORGANISM: Proteus US-09-543-681A-5323

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Query Match 30.6%; Score 48; DB 4; Length 375; Best Local Similarity 52.9%; Pred. No. 22; Matches 9; Conservative 4; Mismatches 4; Indels
                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTARRE: Parentin Release #1.0; Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,433

FLING DATE: 04-MAX-1998

CLASS!FICATION NUMBER: 32,837

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: 32,837

REFERENCE/DOCKET NUMBER: 32,837

REFERENCE/OMMUNICATION INFORMATION:

TELEPRAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 18:

SERVENCE SEQ ID NO: 18:

SERVENCE SEQ ID NO: 18:

SENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Summers, R.G.
APPLICANT: Staver, L.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 111nois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
                  STREET: 220 mouses
CITY: San Francisco
CITY: California
CATTE: California
CATTE: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08576626A; Patent No. 5998194; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||| || || || 244 TVGWPLQPILDNIEHLI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SVGWRLQNIGDDMDHAI 20
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATCAREY/AGENT INFORMATION:
NAME: Dianne Casuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-072-433-18
                                    CITY: Sc. STATE: Califo COUNTRY: University of 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-576-626A-31
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
CHIEF OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REPERBNCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
LENGTH: 579
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| GENERAL INFORMATION: General APPLICANT: Coschigano, Peter | APPLICANT: Coschigano, Peter | TILE OF INVENTION: Compositions and Methods for Bioremediation | TILLE OF INVENTION: Compositions and Methods for Bioremediation | FILE REFERENCE: OHU-03640 | CURRENT FILING DATE: 2001-06-15 | PRIOR PILING DATE: 1998-05-04 | NUMBER OF SEQ ID NOS: 58 | SOFTWARE: 1998-05-04 | NUMBER OF SEQ ID NOS: 58 | SOFTWARE: Patentin version 3.0 | SEQ ID NO 33 | LENGTH: 375 | TYPE: PRT | TYPE: PRT | TYPE: PRT | CREANISM: Thauera aromatica | US-09-323-872A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.6%; Score 48; DB 3; Length 375; Best Local Similarity 52.9%; Pred. No. 22; Matches 9; Conservative 4; Mismatches 4; Indels
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| Patent No. 6551814
| CENERAL INFORMATION:
| APPLICANT: Coschigano, Peter W. TITLE OF INVENTION: CONFOSITIONS AND METHODS FOR INTITLE OF INVENTION: BIOREMEDIATION MUMBER OF SEQUENCES: 42
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                               5-09-198-452A-918
Sequence 918, Application US/09198452A
Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 GWKIECIGDDIAWIRPGRDGRL 281
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US-09-323-872A-33
Sequence 33, Application US/09323872A
Patent No. 6395539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GWRLONIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TVGWPLQPILDNIEHLI 260
                              1 FVRSVGWRLQNIGDDMDH 18
| | | | | | | | | | | 1
71 FTRTVGCPCANIGDHADH 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; Chlamydia pneumoniae; ORGANISM: Chlamydia pneumoniae
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US-09-072-433-18
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Indels

REGISTRATION NUMBER:

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STATE: MASSACHUSEUES
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FLING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/95
FLING DATE: February 4, 1994
CLASSIFICATION NUMBER: 08/192.060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INCORMATION:
NAWE: PAUL T. CLARK
REGISTRATION: MUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
  39.1%; Pred. No. 4.5e tive 3; Mismatches
                                                                                         991 NINWRCDNDNDCGDNSDEAGCSH 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SVGWRLQN---IGDDMDHAICGH 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERA: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 4544 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 8906
TELEFAX: 617 542 8906
  Best Local Similarity 39.1%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-679-279-16
                        Matches
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Patent No. 5739381

GENERAL INFORMATION:

APPLICANT: Thoegersen, Hans Christian
APPLICANT: Elzerodt, Michael

TITLE OF INVENTION: proceins
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
COUNTRY: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 4544;
                                                                                                                                                                                                                                                                                                            Query Match 30.6%; Score 40; DB 2; Length 1114; Best Local Similarity 34.8%; Pred. No. 75; Matches 8; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCIAD NOTES. 30,100
REFERENCIAD NOTES. 30,100
REFERENCIAD INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 52:
LENGTH: 4544 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.3%; Score 47.5;
                 REFERENCE/DOCKET NUMBER: 5857.US.O1
TELECOMUNICATION INFORMATION:
TELEFHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                              16 IRGLHWGYGSNGDPYPMLLCGHD 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                 2 VRSVGWRLQNIGDDMDHAICGHD 24
P-40,943
                                                                                                                   INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 5998194e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                    US-08-576-626A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-469-486-52
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Gaps
Sequence 52, Application US/08469658
Patent No. 5917018
Patent No. 5917018
Patent No. 5917018
Patent No. 5917018
Patent InfoRMATION:
APPLICANT: The gersen, Hans Christian
APPLICANT: Etzerodt, Michael
PITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: IMPROVED
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.3%; Score 47.5; DB 2; Length 4544; Best Local Similarity 39.1%; Pred. No. 4.5e+02; Matches 9; Conservative 3; Mismatches 8; Indels 3.
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Sequence 25635, Application US/09252991A

TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERRINGE: 10799-02-18

FRICK REPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25635

LENGTH: 934
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| GENERAL INFORMATION:
| APPLICANT: Huang, Ziwei
| APPLICANT: Analy, Zhijia |
| APPLICANT: Zhang, Zhijia |
| APPLICANT: Zhang, Zhijia |
| APPLICANT: Zhang, Zhijia |
| APPLICANT: Shan, Simei |
| TILE REFERENCE: 8321-66 |
| CURRENT APPLICATION NUMBER: US/09/544,664B |
| CURRENT FILING DATE: 2000-04-06 |
| PRIOR APPLICATION NUMBER: ECT/US00/09352 |
| PRIOR APPLICATION NUMBER: 60/128,202 |
| PRIOR FILING DATE: 1999-04-07 |
| NUMBER OF SEQ ID NOS: 58 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 15 |
| LENGTH: 27 |
| CONTRIBUTED |
| CONTRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
29.9%; Score 47; DB 4; Length 934;
Best Local Similarity 40.0%; Pred. No. 88;
Matches 10; Conservative 5; Mismatches 10; Indels
                                                             DB 4; Length 465; 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%; Score 46; DB 4; Length 27;
                                                                                                                                      3; Indels
                                                                                                                                  4; Mismatches
                                                                     Score 47;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-544-664B-15
; Sequence 15, Application US/09544664B
; Patent No. 6713280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                        53.38;
                                                                                                                                                                                                                                            || || || |:::| ||:
276 RSEGWNLESLGLDMN 290
                                                                                                                                                                                                           3 RSVGWRLQNIGDDMD 17
                                                                     Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-25635
       US-09-252-991A-16662
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Sequence 16662, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6796, Application US/09328352

Sequence 6796, Application US/09328352

BENERAL INFORMATION:
APPLICANT GATY L. BECON et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6796
LENGTH: 366
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TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic;
TITLE OF INVENTION: Genes and Uses Thereof
FILE REPERENCE: 300622004700
CURRENT APPLICATION NUMBER: US 09/679,279
CURRENT PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/158,305
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
29.9%; Score 47; DB 4; Length 366;
Best Local Similarity 34.6%; Pred. No. 30;
Matches 9; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
29.9%; Score 47; DB 4; Length 358;
Best Local Similarity 34.8%; Pred. No. 29;
Matches 8; Conservative 4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Micromonospora megalomicea
US-09-679-279-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VRSVGWRLQNIGDDMDHAICGHD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-252-991A-16662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-328-352-6796
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MCRUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTRIBUTED: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-5EP-1997
CLASSIFICATION NUMBER: 14
ATTOREY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R:
CRESTERNOE/DOCKET NUMBER: 35,197
REGISTRATION NUMBER: 35,197
REGISTRATION NUMBER: 37,197
TELEPHONINICATION INFORMATION:
TELEPHONINICATION INFORMATION:
TELEPHONINICATION OF SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 10, 2004, 15:57:18 Job time : 12.9537 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VRSVGWRLQNIGDDMDHAI 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 42.1*
....hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-55
                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                       Gaps
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                       ó
                                                                                                                                                                                                          US-08-706-7418-56

1 Sequence 55, Application US/08706741B

1 Patent No. 595593

2 GENERAL INPORMATION:

1 TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

NUMBERS OF SEQUENCES: 88

CORRESPONDENCE ADDERSS:

ADDRESSEE: HOWELL & HAPERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOUR

CONTRY: USA

ZIP: 63146

COMPUTER: ED POSON:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,741B

FILING DATE: 09-SEP-1996

CLASSIFICATION INDER: 35.197

REFERENCE/DOCKET NUMBER: 965017

TELEFONMICATION INFORMATION:

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

TENERAL: 32 Amino of eids
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US-08-924-55
US-08-924-655, Application US/08924695A
; Sequence 55, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2; Length 32;
Pred. No. 2.6;
                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
Best Local Similarity 42.1%; Pred. No. 2.1;
Matches 8; Conservative 4; Mismatches
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29.3%;
Best Local Similarity 42.1%;
Matches 8; Conservative
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-706-7418-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63105
COMPUTER READABLE FORM:
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Gaps

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7; Indels

4; Mismatches

Score 46; DB 2; Length 32; Pred. No. 2.6;

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November 11, 2004, 02:43:24 ; Search time 67.6584 Seconds (without alignments) 146.426 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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157
1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Score Match Length DB ID Description

1 157 100.0 28 14 US-10-092-750-64 Sequence 64, Appl 2 61 38.9 381 17 US-10-739-930-7444 Sequence 7444, Appl 2 61 38.2 526 15 US-10-424-510 Sequence 247510, 3 60 38.2 526 15 US-10-424-510 Sequence 247510, 5 5 5 37.6 148 15 US-10-424-599-247510 Sequence 235298, 6 59 37.6 33.2 17 US-10-739-930-9393 Sequence 246092, 8 54 34.4 1551 11 S US-10-424-599-24856 Sequence 246092, 8 54 34.4 1551 11 S US-10-424-599-24856 Sequence 246092, 8 54 34.4 1551 11 S US-10-424-599-18856 Sequence 153311, 15 33.8 264 14 US-10-424-599-153311 Sequence 153311, 15 33.8 264 14 US-10-369-493-8112 Sequence 137212, Appl 2 53.5 32.8 374 16 US-10-437-963-137212 Sequence 137212,

Sequence 5, Appli Sequence 9, Appli Sequence 28, Appl Sequence 218, Appl Sequence 1035, Ap Sequence 1035, Ap Sequence 10475, Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 31, Appli Sequence 32, Appli Sequence 26, Appli	L-X1 Length 28; Indels 0; Gaps 0;
2.5 606 10 US-09-272-975-5 2.2 605 16 US-10-367-094-9 1.8 253 15 US-10-367-094-9 1.8 579 15 US-10-369-662-918 1.8 605 14 US-10-369-662-918 1.8 605 14 US-10-369-663-1687-5 1.9 605 14 US-10-369-663-1687-5 1.2 295 16 US-10-477-663-16677-5 1.2 295 16 US-10-477-663-16677-5 1.2 534 15 US-10-425-114-5171 0.9 257 16 US-10-425-114-5171 0.9 190 15 US-10-425-114-517-6 0.6 208 17 US-10-425-114-582-8 0.6 223 10 US-09-205-688-213 0.6 223 10 US-09-205-689-3 0.6 375 15 US-10-425-114-806 0.6 375 15 US-10-369-493-8789 0.6 375 15 US-10-369-493-8789 0.7 10-25-114-41806 0.8 10 US-09-750-972-41 0.9 11 US-09-750-972-36 0.1 US-09-750-972-36 0.3 11 US-09-750-972-36 0.3 16 11 US-09-750-972-38	ALIGNMENTS  2750  10/092,750  774,526 ergion 4.0  Score 157; DB 14; Pred. No. 8.1e-16; ; Mismatches 0; CGHDVRLG 28  [        CGHDVRLG 28
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-10-092-750-64 US-10-092-750-64 Sequence 64, Application US/1009 Publication No. US20030032157A1 GENERAL INFORMATION: APPLICANT: Hammond, Philip W. APPLICANT: Alpin, Julia APPLICANT: Alpin, Martin C. TITLE REFERENCE: 50036/050020. CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 2002-03-06 PRIOR APPLICATION NUMBER: US 60; PRIOR APPLICATION NOWER: US 60; PRIOR APPLICATION NUMBER: US 61; CORSENTATION STREET DATE CORSENTATION STREET LOCAL SIMILATION US/10  RESULT 2 US-10-739-930-7444 SEGUENCE 7444, APPLICATION US/10 ; PUDLICATION NO. US20040216190A1; GENERAL INFORMATION:

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 148
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TITLE OF INVENTION: DULBUTE ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(5337)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 9193
LENGTH: 332
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Pred. No. 2.8;
4; Mismatches 8; Indels
                                                                                                                                                                                                          Length 532;
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                                                                                                                                                                                                                                                             9; Indels
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US-10-424-599-235298
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US-10-739-930-9193
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                                                                                                                                                                                                          Query Match 38.2%; Score 60; DB 15; Best Local Similarity 54.5%; Pred. No. 3.2; Matches 12; Conservative 1; Mismatches 9
                                                                                                                                ; OTHER INFORMATION: Clone ID: 700953440_FLI.pep
US-10-425-114-49445
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-10-424-599-235298
US-10-424-599-235298
Sequence 235298, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 42.9%;
Matches 9; Conservative
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ORGANISM: Glycine max
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US-10-739-930-9193
  SEQ ID NO 49445
LENGTH: 532
                                                                                                          FEATURE:
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Publication No. US20040031072A1

Sequence 247510, Application US/2044031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF ESQ ID NOS: 285684

SEQ ID NO 247510
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(5.3377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 7444
LENGTH: 381
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Pred. No. 1.6;
1; Mismatches 9; Indels
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                                                                                                                                                                                                                                                           ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: ZEAWA-23APR03-C152384_1.p
US-10-739-930-7444
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US-10-424-599-247510
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Best Local Similarity 54.5%; Pred. No. 3.2;
Matches 12; Conservative 1; Mismatchen
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Best Local Similarity 52.4%;
Matches 11; Conservative
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US-10-42-115-286505

(S-10-42-115-286505, Application US/10425115

(Sequence 286505, Application US/10425115

(SENERAL INFORMATION:
(APPLICANT: La Rosa, Thomas J.
(APPLICANT: La Rosa, Thuas J.
(APPLICANT: Thou, Yihuas J.
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Publication No. US2040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Avoil of the tension of the tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tension of tens
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34.4%; Score 54; DB 17; Length 1551;
Best Local Similarity 42.1%; Pred. No. 73;
Matches 8; Conservative 7; Mismatches 4; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_109464C.1.pep
US-10-424-599-153311
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; ORGANISM: Zea mays
; PEATURE:
; CTHER INFORMATION: Clone ID: MRT4577_24390C.1.pep
US-10-425-115-286505
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APPLICANT: Zamidio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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ORGANISM: Glycine max
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US-10-282-122A-50976
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US-10-424-599-153311
                                                                                                                                                                                                                                                                                                         Sequence 246092, Application US/10424599

Sequence 246092, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENCE: 38-21(5323) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 246092

LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8

US-10-424-599-218856

US-10-424-599-218856

US-10-424-599-218856

Sequence 218856, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 218856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.0%; Score 55; DB 15; Length 341; Best Local Similarity 38.1%; Pred. No. 11; Matches 8; Conservative 4; Mismatches 9; Indels
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US-10-424-599-218856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_64251C.1.pep
US-10-424-599-246092
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LOCATION: (1)..(479)
CHER INFORMATION: unsure at all Xaa locations
PEATURE:
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                                                                       221 FAEKVGWKIQKRDEDLIHEIC 241
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     1 FVRSVGWRLQNIGDDMDHAIC 21
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Excellic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
ITLE OP INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
ITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137212
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                               Query Match 33.8%; Score 53; DB 14; Length 604; Best Local Similarity 45.5%; Pred. No. 39; Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 606;
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Sequence 5, Application US/09272975

Publication No. US20030027774A1

GENERAL INPORMATION:
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: OF USE THEREFOR
TITLE OF INVENTION: OF USE THEREFOR
CURRENT APPLICATION NUMBER: US/09/272,975

CURRENT APPLICATION NUMBER: US/09/272,975

CURRENT FILING DATE: 1999-03-18

NOTHARE OF SEQ ID NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH. 606
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US-10-437-963-137212
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                                                                                                                                                                                                                                                                                                                                                           Sequence 137212, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                         S VGWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 VEWEFKSLEDGKWHA-CGHDVHV 77
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US-09-272-975-5
                                                                                                                                                  6 GWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-437-963-137212
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Sequence 812, Application US/10369493

Publication No. US2030323675A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GOUGHAIN Cao, Yongwei

APPLICANT: Gare, Yongwei

APPLICANT: Goldman, Barry
APPLICANT: Goldman, Barry

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374

SEQ ID NO 8112

LENGRIH: 604
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PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR APPLICATION NUMBER: 60/230, 335

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-110-23

PRIOR PELING DATE: 2000-110-22

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-16

                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms File REPERDICE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 VRSMOWHSVNVPRDPDCAVCG 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.1
SEQ ID NO 50976
LENGTH: 264
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; ORGANISM: Thermobifida fusca
US-10-369-493-8112
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                         Trawick, John
Carr, Grant
Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserve
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US-10-282-122A-50976
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RESULT 15
US-10-367-094-9
19-287 GWRAETLGDDIAMWRFGKDGRL 308

RESULT 15
US-10-367-094-9
19-261-0-367-094-9
19-261-0-367-094-9
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Search completed: November 11, 2004, 07:41:44 Job time : 67.6584 secs

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- protein search, using sw model OM protein

Run on:

November 10, 2004, 14:52:32; Search time 9.56584 Seconds (without alignments) 281.634 Million cell updates/sec

US-10-092-750-64

157 1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28 Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PiR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	probable pckA prot	phosphoenolpyruvat	probable phosphoen	hypothetical prote	frcB protein (AF19	probable phosphoen	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	probable potassium	hypothetical prote		Н	splicesome-associa	phosphoenolpyruvat	hypothetical prote	hydroxyacylglutath	ornithine carbamoy	transcription fact	alpha-2-macroglobu	alpha-2-macroglobu	alpha-2-macroglobu	probable acetyltra	hypothetical prote	lipoamide dehydrog	900	probable L-a-amino	)le	je S
ΩI	A70960	F87237	m	AB2584	B97366	4	E72027	A86597	JQ1462	C72692	G96940	G83689	C84563	T40304	A45625	T24168	AB3314	F82737	T10695	A53102	802392	S25111	C75096	AB1943	F83365	C83358	S72728	AB0106	G70817
Length DB	606 2		618 2																			545							
강당	ı N	N	32.5	н	<b>7-1</b>	-1	-1	-1	н	Н	$\leftarrow$	0	0	0	О	0	0	0	O	0	0	0	O)	σ	σ	g	σ	g	O)
Score	512	51	51	20	20	20	20	20	20	49	49	48	48	48	48	48		47.5		47.5		•	47	47	47	47	46	46	46
Result No.		7	е	4	Ŋ	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

naringenin-chalcon	NADH oxidase SS019	heat shock protein	phosphoenolpyruvat	hypothetical prote	fibulin, splice fo	fibulin, splice fo	SpoE family protei	cell division prot	gene 44 protein -	amino acid amidohy	Ig lambda chain pr	bacterioferritin c	conserved hypothet	probable f0-f0 par	MRP protein homolo
S44367	D90354	C83168	830180	T32875	S78040	S34968	D95101	E97969	WZBE44	B86660	A30554	B82742	E81672	T38680	A90191
N	~	N	7	7	N	~	0	7	~	~	~	N	~	N	N
389	555	619	646	651	685	705	767	167	363	384	129	159	178	286	296
29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.0	29.0	28.7	28.7	28.7	28.7	28.7
46	46	46	46	46	46	46	46	46	45.5	45.5	45	45	45	45	45
30	31	32	33	34	35	36	37	38	99	40	41	42	43	4.4	45

# ALIGNMENTS

RESULT 1

A70960	
probable pckA protein - Mycobacterium tuberculosis (strain H37RV)	
C;Species: Mycobacterium tuberculosis	
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004	
C,Accession: A70960	
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,	don,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S	yd, s
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	
Nature 393, 537-544, 1998	
A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	enome
A; Reference number: A70500; MUID: 98295987; PMID: 9634230	
A;Accession: A70960	
A; Status: preliminary; nucleic acid sequence not shown; translation not shown	
A; Molecule type: DNA	
A;Residues: 1-606 <col/>	
A; Cross-references: UNIPROT: P96393; GB: Z92669; GB: AL123456; NID: 93242271; PIDN: CAB07006	90000
A:Experimental source: strain H37Rv	

A,Experimental source: strain H37Rv C,Genetics: A,Gene: pockA C,Superfamily: phosphoenolpyruvate carboxykinase (GTP)

ö Gaps ö Ouery Match 32.5%; Score 51; DB 2; Length 606; Best Local Similarity 45.5%; Pred. No. 13; Matches 10; Conservative 3; Mismatches 9; Indels

||| ::|||: 287 GWRAETLGDDIAWMRFGKDGRL 308 6 GWRLQNIGDDMDHAICGHDVRL 27 ద ઠ

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from protein (AF196574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97366
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Curollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97366
A;Status: preliminary
A;Molecule type: DNA
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C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence = revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: G71481
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell A;Tite: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tracellular preliminary
A;Accession: G71481
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A,Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-340 <KUR>
A;Cross_references: UNIPROT:Q8UJ75; GB;AE007869; PIDN:AAK85883.1; PID:g15154926; GSPDB:
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Saccession: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C; Accession: E72001; W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1599
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
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C,Superfamily: phosphoenolpyruvate carboxykinase (GTP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2;
Pred. No. 9.9;
2; Mismatches 8
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31.8%; Score 50; DB
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 5; Mismatches
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A,Map position: circular chromosome
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Best Local Similarity 50.0%;
Matches 10; Conservative
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A,Molecule type: DNA
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-618 <COL>
A;Cross-references: UNIPROT:O83159; GB:AE001197; GB:AE000520; NID:g3322382; PIDN:AAC6511
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0122
C;Superfamily: phosphoenolpyruvate carboxykinase (GTP)
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A, Molecule type: DNA
A, Residues: 1-340 < KCUR>
A, Cross-references: UNIPROT: Q8UJ75; GB: AE008688; PIDN: AAL41088.1; PID: g17738379; GSPDB: G
A, Experimental source: strain C58 (Dupont)
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2.317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A71364
Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID: 98332770; PMID: 9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein frcB [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #text_change 09-Jul-2004
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable phosphoenolpyruvate carboxykinase (pckA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                Gaps
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                                                                               Query Match 32.5%; Score 51; DB 2; Length 609; Best Local Similarity 45.5%; Pred. No. 13; Matches 10; Conservative 3; Mismatches 9; Indels
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C; Superfamily: phosphoenolpyruvate carboxykinase (GTP)
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31.8%; Score 50; DB 2
Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 10; Conservative 2; Mismatches
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hypothetical protein BH0319 [imported] - Bacillus halodurans (strain C-125)

C,Species Bacillus halodurans
C,Species Bacillus halodurans
C,Accession: G83689

R,Tatkami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Recference number: A83650; MUID:20512582; PMID:11058132
A,Accession: G83689
A,Status: preliminary
A,Nolecule type: DNA
A,Residues: 1-108 < STOAD
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A;Experimental source: Clostridium acetobutylicum ATCC824
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3; Mismatches
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5; Mismatches
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nes 10; Conservative
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A,Molecule type: DNA
A,Residues: 1-786 <KUR>
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A;Accession: A86597
A;Accession: A65597
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-600 <STDO.
A;Accessive references: UNIPROT:092755; GB:BA000008; NID:g8979225; PIDN:BAA99059.1; GSPDB:GN
A;Experimental source: strain J138
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C;Species: Neocallimastix frontalis
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
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A,Residues: 1-600 <ARN>
A;Cross-references: UNIPROT:Q9Z755; GB:AE001666; GB:AE001363; NID:g4377164; PIDN:AAD1898
A;Experimental source: strain CWL029
C;Genetics:
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C;Accession: JQ1462
R;Reymon; JQ1462
R;Reymon; JG0urjon, C.; Roux, B.; Durand, R.; Fevre, M.
Gene 110, 57-63, 1992
A;Title: Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from the rumen A;Title: Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from the rumen A;Reference number: JQ1462, MUID:92184115, PMID:1339359
A;Accession: JQ1462
A;Molecule type: mRNA
A;Residues; 1-608 <REYS
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R.Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; E. Nucleic Acids Res. 28, 2311-2314, 2000
A.Title: Comparison of Whole genome sequences of chlamydia pneumoniae J138.
A.Reference number: A86491; MUID:20330349; PMID:10871362
A.Accession: A86597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 2; Length 600;
Pred. No. 18;
4; Mismatches 8; Indels
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                                                                                            A;Cross-references: UNIPROT:Q9%/35; GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1809, GB:ABUV1909, GB:ABUV1909, GB:ABUV1909, GB:ABUV1909, GB:ABUV1909, GB:ABUV1809, GB:ABUV1
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C, Superfamily: phosphoenolpyruvate carboxykinase
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31.8%; Score 50; DB
Best Local Similarity 40.9%; Pred. No. 18;
Matches 9; Conservative 5; Mismatches
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GWKIECIGDDIAWIRPGRDGRL 302
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ilarity 45.5%;
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Best Local Similarity 45.5%;
Matches 10; Conservative
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Matches 10; Conserv
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: C84563
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Ribyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Duesterh submitted to the EMBL Data Library, May 1998

A;Reference number: 221919

A;Accession: T40304

A;Accession: T40304

A;Accession: T4030

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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                      Query Match 30.6%; Score 48; DB 2; Length 108; Best Local Similarity 44.0%; Pred. No. 5.8; Matches 11; Conservative 3; Mismatches 7; Indels
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33.3%; Pred. No. 15;
ive 4; Mismatches 10; Indels
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Best Local Similarity 33.3%
Matches 7, Conservative
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A,Map position: 2
C;Genetics:
A;Gene: BH0319
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C;Accession: A45625
R;Klein, R.D.; Winterrowd, C.A.; Hatzenbuhler, N.T.; Shea, M.H.; Favreau, M.A.; Nulf, S
Mol. Biochem. Parasitol. 50, 288-294, 1992
A;Title: Cloning of a cDNA encoding phosphoenolpyruvate carboxykinase from Haemonchus of A;Reference number: A45625, MUID:92158009; PMID:1741016
                                                                                                                                                                                                                                                                                                                           A;Accession: A45625
A;Btatus: preliminary
A;Molecule type: mRNA
A;Reaidues: 1-619 < KLE>
A;Cross-references: UNIPROT:P29190; GB:M76494; NID:g159182; PIDN:AAA29180.1; PID:g15918:
A;Cross-references: UNIPROT:P29190; GB:M76494; NID:g159182;
A;Note: sequence extracted from NCBI backbone (NCBIN:83527, NCBIP:83529)
C;Superfamily: phosphoenol.pyruvate carboxyxinase (GTP)
C;Keywords: carbon-carbon lyase; carboxy-lyase; gluconeogenesis
- nematode (Haemonchus contortus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                          C;Species: Haemonchus contortus
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
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phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32)
N/Alternate names: phosphoenolpyruvate carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 10, 2004, 15:55:02 Job time : 10.5658 secs
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Best Local Similarity
Matches 9; Conserv
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RESULT 15 A45625 Н

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 46.9324 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

US-10-092-750-64 157 1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		Description	4 gordonia	_	Ó	Q7vs40 bordetella			Q9agj6 mycobacteri	Q6f8p2 acinetobact				7 ory	P96393 mycobacteri						Q80py9 suid herpes	Q99m67 mus musculu	Q7tmw0 mus musculu	P56690 thermus the	Q72jr6 thermus the	Aas81050 thermus t	Q98pa4 rhizobium l	83×m9	7d298	Q8uj75 agrobacteri	881k0		
SUMMAKLES	-	ΔI	Q70K64	CAE09117	Q874G3	Q7VS40	Q7W1Q3	Q7WQM9	PPCK MYCSM	Q6F8 <u>P</u> 2	QBIHKB	Q86JG5	Q851L5	AAR88567	PPCK MYCTU	PPCK_MYCLE	Q73TS2	AAS06196	PPCK TREPA	Q98SW5	Q80PY9	Q99M67	Q7TMW0	SYI THETH	Q72JR6	AAS81050		Q83XM9	Q7D298	Q8UJ75	QBBLKO	PPCK_CHLTR	PPCK_CHLPN
		DB	N	N	N	N	N	~	Н	~	N	N	N	~	-	7	0	N	Н	~	~	~	~	Н	0	~	7	~	0	0	~	Н	н
		Length	230	230	1067	264	264	264	605	609	2507	2929	417	417	909	609	609	609	618	814	328	601	602	821	1067	1067	202	253	340	340	478	599	600
d	Query	~ !	α	38.9	4.	33.8	÷	ش	۳.	33.1	ω.	<u>.</u>	ς.	ď.	ď	ς.	ς,	'n	ď.	ď	'n	ä	ö	'n	'n	o,		ä	ä	31.8		ä	ij
		Score	ч	61	54	53	53	23	52	52	25	52	51.5	ä	51	51	51	51	51	Ŋ	ö	。	ö	50.5	。	。	20	20	20	20	20	20	000
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Q82171 streptomyce P22130 neocallimas Q9315 streptomyce Q7n6x2 photorhabdu Q94f8 arcopyrum p Q985p8 rhizobium 1 Q6mbf4 parachlamyd Caf24095 parachlamyd Caf24095 parachlamyd G6f880 erwinia car Q86906 mus musculu Q89f99 bradyrhizob Q7xtv7 oryza sativ Q87£7 bacillus ha
PPCK_STRAW PPCK_NEOFR PPCK_STRCO Q7N6X2 Q7N6X2 Q8085F4 Q8085F4 Q8085F6 Q97865 Q97865 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9U6 Q8C9 Q8C9 Q8C9 Q8C9 Q8C9 Q8C9 Q8C9 Q8C9
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# ALIGNMENTS

PRESIDENT 1  OTOK64  PRELIMINARY; PRT; 230 AA.  DG 070K64  DG 070K10-2004 (TrEMBLrel. 27, Last sequence update) DG 070K10-2004 (TrEMBLrel. 27, Last sequence update) DG 05-ULD-2004 (TrEMBLrel. 27, Last sequence update) DG 05-ULD-2004 (TrEMBLrel. 27, Last annotation update) DG 05-ULD-2004 (TrEMBLrel. 27, Last annotation update) DG 05-ULD-2004 (TrEMBLrel. 27, Last annotation update) DG 05-ULD-2004 (TrEMBLrel. 27, Last annotation update) DG 05-ULD-2004 (TrEMBLrel. 27, Last annotation update) DG 05-ULD-2004 (TREMBLRel. 27, Last annotation update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last sequence update) DG 05-ULD-2004 (TREMBLREL. 27, Last annotation update) DG 05-ULD-2004 (TREMBLREL. 27, Last annotation update) DG 05-ULD-2004 (TREMBLREL. 27, Last annotation upd
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NCBI_TaxID=520;
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                                                   RESULT 4
Q7VS40
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003671; F:DNA binding; IEA.
GO; GO:00046519; F:endonuclease activity; IEA.
GO; GO:0046693; F:hydrogen-transporting ATP synthase activity. .; IEA.
GO; GO:0016986; P:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0019986; P:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0019986; P:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0019986; P:hydrogen-transporting ATPase activity, rota. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okuda Y., Sasaki D., Nogami S., Kaneko Y., Ohya Y., Anraku Y.; "Occurrence, horizontal transfer and degeneration of VDE intein family in Saccharomycete yeasts."; Sasat 20:563-57312003.
-! SIMILARITY: Belongs to the ATPase alpha/beta chains family.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=34358;
                            Broeker D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ576039; CAE09117.1; -.
Helicase; Hypothetical protein; Lipoprotein; Methyltransferase;
                                                                                                                                                       ö
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                                                                                                                     / Match
Local Similarity 45.8%; Pred. No. 0.96;
les 11; Conservative 3; Mismatches 10; Indels
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                                                                                              230 AA; 25736 MW; 929260575B53D0F2 CRC64;
                                                                                                                                                                                                                                                                                                           01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07N-2004 (TrEMBLrel. 26, Last annotation update)
Vacuolar membrana ATPase subunit a 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF05203; Hom_end hint; 1.
PROSITE; PS00152; ATPASE ALPHA BETA; UNKNOWN_1.
PROSITE; PS50819; INTEIN ENDONUCLEASE; 1.
                                                                                                                                                                                                                                                                                 PRT; 1067 AA
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InterPro; IPR00194; AIPase a/b.C.
InterPro; IPR00199; AIPase a/b.C.
InterPro; IPR007869; Hom end.
InterPro; IPR007869; Hom end hint.
IPEam; PP00306; AIP-synt ab; I.
Pfam; PP09306; AIP-synt ab; I.
Pfam; PP05204; Hom end; I.
Pfam; PP05204; Hom end hint; I.
                                                                                                                                                                                                  | | | | : | | | | : | | 130 FCRGCGWHSEVVGDDTDAALLGLD 153
                                                                                                                                                                                   1 FVRSVGWRLQNIGDDMDHAICGHD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22620229; PubMed=12734795;
                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces exiguus (Yeast)
SEQUENCE FROM N.A.
STRAIN=type strain: DSM44215;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE
                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                 Q874G3
Q874G3;
                                                                                    Plasmid
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Matches
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SEQUENCE FROM N.A.

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MINIMATOR AND SEQUENCE 12910271; DOI=10.1038/ng1227;

MEDINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Rackhon M., Araraga A. A., Temple L., James K.D., Harris B., Quail M.A.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Feltwall T., Goble A., Hamlin N., Hauser H., Holloyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

The Bordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
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Alcaligenaceae, Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Genet. 35:32-40(2003).
EMBL, BX464012; CR544936.1; -.
GO; GO:0016779; F:nuclectidyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome, Nucleotidyltransferase, Transferase, SEQUENCE 264 AA; 28007 MW; CASBB10EFEC3D944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7W1Q3;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Adenylyltransferase (EC 2.7.7.-).
                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Adenylyltransferase (EC 2.7.7.-).
Name-thif; OrderedLocusNames=BP0610;
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                                                                                                                                                                                                                                                                                                               264 AA
662 RSLGIKITVTSDDSDDSDEHDHAHGGHD 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007901; MoeZ MoeB.
InterPro; IPR002205; MAD BS.
InterPro; IPR000594; ThiF domain.
Pfam; PF05237; MoeZ MoeB; 1.
Pfam; PF06899; ThiF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
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Les 10; Conservative
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Pred. No.

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PSECURATE FROM N.A.

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SEATIN=E850 / ATCC BAA-588;

NEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

Rathill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A cerdeno-Tarraga A.-M., Temple J., James K.D., Bavis P., Doggett J.,

A chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A cerdeno-Tarraga A.-Mamiin N., Hauser H., Holroyd S., Jagels K.,

A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Rabbinowitsch B., Rutter S., Sanders R., Squares S., Stevens K.,

Rabbinowitsch B., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Rabbinowitsch B., Sanderla B.G., Maskell D.J.,

RA Dawin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

R sonderella parapertussis and Bordetella bronchiseptica.";
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chilingworth T., Collins M., Croint A., Davis P., Dogett J., Athilingworth T., Collins M., Croint A., Davis P., Dogett J., Collins M., Cloint A., Davis P., Dogett J., Cathwell T., Coble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Sharbinowitsch E., Rutter S., Sanders B., Seeger K., Asbinowitsch E., Whitehead S., Sanders B., Seeger K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J., Geger K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J., Geger K., Comparative analysis of the genome sequences of Bordetella pertussis, R. Mat. Genet. 35:32-40(2003).

Bordetella parapertussis and Bordetella bronchiseptica.";

BMEL, BX640423; CAE40039.1; -.

GO; GO:0016779; Firansferase activity; IEA.

GO; GO:0016779; Firansferase activity; IEA.

InterPro; IPR007901; Moez MoeB.

InterPro; IPR000504; Thip domain.

Pfam; PP005179; Moez MoeB.

InterPro; IPR00899; Thip domain.

Pfam; PP00899; Thip domain.

Pfam; PP00899; Thip domain.
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
11-0CT-2003 (TrEMBLrel. 26, Last annotation update)
Adenylyttransferase (EC 2 7.7.7.).
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Pred. No. 17;
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NCBI_TaxID=518;
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nes 10; Conservative
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Q7WQM9
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., CHARACTERIZATION, AND MASS SPECTROMETRY.
MEDLITRE=12138287; PUNAcd=11278451; DOI: 10.074/jbc.M008960200;
MEDLITRE=12282887; PUNAcd=11278451; DOI: 40.016 R.S.;
Mukhopadhyay B., Concar E.W., Wolfe R.S.;
"A GTP-dependent vertebrate-type phosphoenolpyruvate carboxykinase from Mycobacterium megmatis.",
J. Sholl. Chem. 276:16137-16145(2001).
-I. CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
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                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MASS SPECTROMETRY: MW=71209; METHOD=MALDI; RANGE=1-605;
NOTE=Ref.1.
                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (RC 4.1.1.32) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
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                       Indels
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InterPro; IPR008210; PEPCK N.
InterPro; IPR008210; PEPCK N.
Pfam; PF00821; PEPCK; 1.
ProDom; PF004738; PEPCK 1.
PROSTIE; PS00505; PEPCK GIP; 1.
PROSTIE; PS00505; PEPCK GIP; 1.
Decarboxylase; Gluconeogenesis; GIP-binding; Lyase.
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PATHWAY: Rate-limiting gluconeogenic enzyme.
SUBUNIT: Monomer.
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     ed. No. 17;
Mismatches
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287 GWRAETVGDDIAWMRFGKDGRL 308
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                                                                             227 VRSMOWHSVNVPRDPDCAVCG 247
                                                       2 VRSVGWRLQNIGDDMDHAICG 22
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HSSP; P35558; 1KHB.
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                       Conservative
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Mycobacterium smegmatis.
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les 10; Conserva
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE
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RESULT 8 Q6F8P2

Length 264;

DB 2;

33.8%; Score 53;

Query Match

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SMART; SM00320; WD40; 2
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Best Local Similarity
9; Conserve
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NON TER 1
SEQUENCE 2507 AA;
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MEDLINE=2198669; PubMed=12210762;

MEDLINE=2198669; PubMed=12210762;

MEDLINE=2198669; PubMed=12210762;

MEDLINE=2198669; PubMed=12210762;

MEDLINE=2198669; Proteins: phylogenetic and functional analysis of six Dictyostellium BEACH proteins: phylogenetic and functional analysis of six Dictyostellium BEACH proteins: phylogenetic and functional analysis of six Dictyostellium BEACH proteins: phylogenetic and functional analysis of six Dictyostellium BEACH proteins: phylogenetic and function phylogenetic analysis of six Dictyostellium BEACH.

InterPro; IPR000409; Peptidase_226.

InterPro; IPR001680; WD40.

InterPro; IPR00166; WD40.

INTERPRO; IPR00166; WD40.

INTERPRO; IPR00166; WD40.
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                                                                                                                                                                                                                                                                                                     Darbe V., Vallent D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Cornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C., "Unique features revealed by the genome sequence of Acinecobacter sp. ADPI, a versatile and naturally transformation competent bacterium."; Nucleic Acids Res. 0.0-0(2004).

EMBL, CR543861, CAG69573.11 --.
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                                                                                                                                 Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellacae; Adinetobacter.
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Harris E., Wang N., Wu Wl W.L., Weatherford A., De Lozanne A.,
Cardelli J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 609;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
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PROSITE; PS00505; PEPCK_GTP; 1.
Complete protecome; Kinase; Lyase; Pyruvate.
SEQUENCE 609 AA; 67306 MW; 5301EBFB66E3231E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostejium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphoenolpyruvate carboxykinase (EC 4.1.1.32).
Name=pckG; OrderedLocusNames=ACIAD2842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2507 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.1%; Score 52; DB Best Local Similarity 40.9%; Pred. No. 58; Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR008210; PEPCK N.
InterPro, IPR008209; PEP carboxykin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 GWKIETVGDDIAWIKPGEDGRL 306
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GWRLONIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with Chediak-Higashi syndrome.";
Mol. Biol. Cell 13:656-669(2002)
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR008209; PEF
Pfam; PF00821; PEPCK; 1.
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                         Q6F8P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8IHK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
Q81HK8
     DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner G., Eichinger L., Száfranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzar M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                         Length 2507;
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                                                                                                                                                                                                                                                                Query Match 33.1%; Score 52; DB 2; Length 250
Best Local Similarity 42.9%; Pred. No. 2.5e+02;
Matches 9; Conservative 4; Mismatches 8; Indels
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                                                                                                                                                          1 1 2507 AA; 283343 MW; 3821DD88B23CE476 CRC64;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  %00-003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNA-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). LvsD.
Dictyostelium discoideum (Slime mold). EvsD.
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
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OBSILS;
O1-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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FIGSP: ARCIT 6982; AAO51610.1; ---
HASP: QRNPP9; IMI.
HASP: QRNPP9; IMI.
HASP: QRNPP9; IMI.
HASP: QRNPP9; IMI.
HASP: PROUGOS PEDTIGASE_S16.
HASP: PROUGOS PEDTIGASE_S26.
PROSTTE; PROUGOS PEDTIGASE_SAMPI.
PROSTTE; PSOUGOS, PROUGOS SAMPI.
PROSTTE; PSOUGOS PAGE II; UNKNOWN I.
REPROSTE; PSOUGOS PAGE III; UNKNOWN I.
REPROSTE; PSOUGOS PAGE II; UNKNOWN I.
REPROUGOS PAGE III; UNKNOWN I.
PROSITE; PS50197; BEACH; 1.
PROSITE; PS00501; SPASE I 1; UNKNOWN 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1016 | | | | | | | | | | 1036
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MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                       7 WRLQNIGDDMDHAICGHDVRL 27
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Teitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Xoo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mite O., Salzberg S.L., Fraser C.M.; M.; G.S., Salzberg S.L., Fraser C.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                           Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092557; AAR88567.1; ...
Hydrolase.
SEQUENCE 417 AA; 43990 MW; 7F1326A1FB883B54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              5 VGWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                  STRAIN=cv. Nipponbare;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                SECUENCE FROM N.A.
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SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Sub B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                          Putative amidohydrolase.

Name=OSJNBa0042I09.29; Synonyms=OSJNBa0096I06.2;

Name=OSJNBa0042I09.29; Synonyms=OSJNBa0096I06.2;

Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overcon Il L.L., Tsiturin T., Kim M.N., Bara J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V. Hsiao J., Blant S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Vanaken S.S., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.V., White O., Salzberg S.L., Fraser C.M.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC104487; AAO41148.1; -.
EMBL; AC092557; AAR86567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 Buell R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 AA; 43990 MW; 7F1326A1FB883B54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; ACCASILS; - GRALES; F. Hydrolase activity; IEA. GRO, GO:0006508; P: proteolysis and peptidolysis; IEA. INTERPRO, IRRO02933; Peptidase_MZO. INTERPRO; IRRO168; Pept MZOD amidh.
          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
32.8%;
Best Local Similarity 43.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                FROM N.A.
                                                                                                                                           NCBI_TaxID=39947;
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Gaps

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Indels

ω ω 5;

4; Mismatches

| | ::: | | || || :: | VEWEFKSLEDGRMHA-CGHDVHV 120

32.8%; Score 51.5; DB 43.5%; Pred. No. 47;

Length 417;

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Capecinis Faccinists; STRAIN=H37RV;

WEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;

MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

A Harris D.E., Gordon S.V., Eiglmedier K., Garden S., Barry C.E. III,

Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares J.,

Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

B Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.;

II Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES—M. tuberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Hickey E.K., Kolonay J.F., Melson W.C., Umayam L.A., Ermolaeva M.D.,
Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                           Name=pckG; Synonyms=pckA, pckl;
OrderedLocusNames=Rv0211, MT0221, Mb0217; ORFNames=MTCY08D5.06;
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                          Mycobacterium bovis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae, Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last amotation update)
Phosphoenolpyruvate carboxykinase [GTP] (RC 4.1.1.32) (PEP
                                                                                                                            carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK)
606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 184:5479-5490(2002)
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
    MYCTU
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Oryza sativa (japonica cultivar-group). Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzee, Oryza, Oryza sativa.

SEQUENCE FROM N.A. STRAIN=cv. Nipponbare;

NCBI_TaxID=39947;

RAPACOCCOS SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICES OF SERVICE

AAR88567; 02-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) Putative anidohydrolase.

PRT;

PRELIMINARY;

AAR88567

RESULT 12 AAR88567

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ProDom; PD004738; PEPCK N; 1.
PROSITE; PS00505; PEPCK GTP; 1.
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                                                                                                                                                                                                                                                           family.
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Q73TS2
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Tuberculist; kvuzıı;

InterPro; 1PR008210; PEPCK_N.

InterPro; IPR008209; PEP arboxykin.

Pfam; PF00821; PEPCK; 1.

Prodom, PF00821; PEPCK; N; 1.

PROSTIE; PS00505; PEPCK GTP; 1.

Complete proteome; Perchoxylase; Gluconeogenesis; GTP-binding; Lyase.
MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                 -!- F CO(2).
-!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBJUIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honoren N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Phosphoenolpyruvate carboxyxinase [GTP] (EC 4.1.1.32) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK)
Name=pcKG; Synonyms=pcKA; OrderedLocusNames=ML2624;
ORFNAmes=MLCL622.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 51; DB 1; Length 606; 45.5%; Pred. No. 82; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 273 By similarity.
606 AA; 67253 MW; ABE29412E6BCCAE3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BX842572; CAB07006.1; --
EMBL; AE006931; AAK4442.1; --
EMBL; BX248334; CAD93081.1; --
PIR; A70950, A70960.
HSSP; P35558; 1XHB.
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Best Local Similarity 45.5%
Matches 10, Conservative
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SEQUENCE
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PPCK_MYCLE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter. S., Seeger K., Simon S., Simons M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G., Moodward J.R., Massive gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001).

-! - CALLYITC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
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Prodom; PF00821; PEPCK N; 1.
Complete Proteome, Decarboxylase; Gluconeogenesis; GTP-binding; Lyase.
NP BIND 2.22 229 229 CM GTP (Potential).
ACT SITE 273 273 By similarity.
SEQUENCE 609 AA; 67731 MW; 891686733622590B CRC64;
                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
-1- SUBONIT: Monomer (By similarity).
-1- SUBCELLULA: LOCATION: (Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
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EMBL; AE017240; AASO6196.1; -.
InterPro; IPR008210; PEPCK N.
InterPro; IPR008209; PEP_Carboxykin.
PF00821; PEPCK; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51, DB 1; Length 609;
Pred. No. 82;
3; Mismatches 9; Indels
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609 AA.
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Best Local Similarity 45.5%; Pred. No. 8
Matches 10; Conservative 3; Mismatcl
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InterPro; IPR008210; PEPCK N.
InterPro; IPR008209; PEP_carboxykin.
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EMBL, ALS8926; CAC32156.1; -
PIR; F87237; F87237.
HSSP, P35558; IKHB.
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0; Gaps
                                                                           Query Match 32.5%; Score 51; DB 2; Length 609; Best Local Similarity 45.5%; Pred. No. 82; Matches 10; Conservative 3; Mismatches 9; Indels
KW Complete proteome.
SQ SEQUENCE 609 Aa; 67659 MW; 8ABF04BFFF2D1847 CRC64;
                                                                                                                                                                                6 GWRLQNIGDDMDHAICGHDVRL 27 | | | | | | | | | 287 GWRAETLGDDIAWRRGKDGRL 308
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Search completed: November 10, 2004, 15:53:22 Job time : 49.0093 secs

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Sequence 23033, A Sequence 23, Appl Sequence 26199, A Sequence 25490, A Sequence 21568, A Sequence 21500, Ap Sequence 21507, Ap Sequence 21011, A Sequence 6, Appli Sequence 6, Appli Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl
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2: /cgm2_6/ptodata1/iaa/5B_COMB.pep:*
3: /cgm2_6/ptodata1/iaa/6A_COMB.pep:*
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5: /cgm2_6/ptodata1/iaa/PcTUS COMB.pep:*
6: /cgm2_6/ptodata1/iaa/PcTUS COMB.pep:*
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US-09-486-393-6

US-08-461-96-506

US-08-486-397-42

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US-09-249-473-42 US-09-252-991A-31721 US-09-252-991A-32998 US-09-252-991A-29948 US-09-252-991A-29948 US-09-252-991A-2467 US-09-252-991A-24667 US-09-252-991A-24667 US-09-252-991A-19069 S183745-4 US-09-252-991A-19069 S183745-6 US-08-669-785-4 US-08-669-785-4 US-08-669-785-7 US-09-020-065A-36 US-09-020-065A-36 US-09-020-065A-36 US-09-020-065A-36	ALIGNMENTS	91A DIAGNOSTICS 2,991A 7,788	Score 41.5; DB 4; Pred. No. 35; 1; Mismatches 1;		THE INTERLEUKIN
44444444444444444444444444444444444444		pplication US/09 pplication US/09 S. ON: U. Rubenfield e. ON: NUCLEIC ACI NOT196.136 107196.136 110N NUMBER: US/0 ATE: 1999-02-18 N NUMBER: US 60 E: 1998-07-18 E: 1998-07-18 N NUMBER: US 60 E: 1998-07-27 NOS: 33142	60.1%; larity 75.0%; Conservative	GSSQ 12    :  GSSR 80	lication US/07%  lichol.  lynor, Richard  lrula, Alay  lrula, Alay  rrion:  rr
20.00		SSULT 1 5.09-252-991A-23033 Sequence 23033, Application US/092529 Patent No. 6551795 Eatent No. 6551795 GENERAL INPORMATION: APPLICANT: Marc J. Rubenfield et al TITLE OF INVENTION: NUCLEIC ACID ANY TITLE OF INVENTION: NUCLEIC ACID ANY TITLE OF INVENTION: APPLICATION NUMBER: US/09/25 CURRENT APPLICATION NUMBER: US/09/25 CURRENT FILING DATE: 1999-02-18 PRIOR FILING DATE: 1999-02-18 PRIOR FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23033 LENGTH: 501 TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: P	imis	2 GLRKP-TCGSSQ           : 69 GFRKPCTCGSSR	JUT 2  30-906-930B-33  equence 33, Application US/0790  atent No. 5534631  SENERAL INFORMATION:  APPLICANT: Gaynor, Richard B  APPLICANT: Li, Ching  APPLICANT: Li, Ching  APPLICANT: Li, Ching  TITLE OF INVENTION: BACTOR  TITLE OF INVENTION: FACTOR  NUMBER OF SEQUENCES: 33  CORRESPONDENCE ADDRESS:  ADDRESSEE: Arnold, White & STRET: P. O. Box 4433  CITY: Houston  STRET: P. O. Box 4433  CITY: Houston  STRIE: Texas  COUNTRY: USA  ZIP: 77210  COMPUTER READABLE FORM:
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-09-252-991A-2303; Sequence 2303; Ap; Patent No. 655179; Patent No. 655179; GENERAL INPORVATION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION FILE REFRENCE: CURRENT APPLICATION DATE OF THE NOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR PRIOR PRIOR DATE OF THE NOR APPLICATION PRIOR PRIOR PRIOR PRIOR DATE OF THE NOR APPLICATION PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	Query Match Best Local 6 Matches	, 60 60 60	RESULT 2 US-07-906-930B-33 Sequence 33, Application US/07906930) Patent No. 5534631 Patent No. 5534631 Patent No. 5534631 Patent No. 5534631 APPLICANT: Gaynor, Richard B. APPLICANT: Gaynor, Richard B. APPLICANT: Nirula, Ajay APPLICANT: Nirula, Ajay APPLICANT: Nirula, Ajay APPLICANT: Nirula, Ajay APPLICANT: Nirula, Ajay APPLICANT: Nirula, Ajay APPLICANT: Normanian DNA ENCODING TITLE OF INVENTION: FACTOR (ILF) NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Duri STREET: P. O. Box 4433 CITY: Houston STREET: Texas COUNTRY: USA ZIP: 77210

Fri Nov 12 14:55:53 2004

), ORGANISM: Drosophila melanogaster US-09-270-767-44530

Score 38; DB 4; Length 65; Pred. No. 19; 5; Indels 0; Mismatches Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative

Gaps

; 0

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Sequence 26199, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSOCIATION ASSOCIATION OF THE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788 RESULT 4 US-09-252-991A-26199

ö Score 38; DB 4; Length 153; Pred. No. 43; 2; Mismatches 2; Indels PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26199
LENGTH: 153 ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26199 55.1%; 60.0%; Ouery Match
Best Local Similarity 60...
Best Gonervative 4 RKPTCGSSOR 13 TYPE: PRT à

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Gaps

87 RRPNCGSCRR 96

Sequence 24968, Application US/09252991A Patent No. 6551795 JS-09-252-991A-24968

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Gaps

.; 0

2; Indels

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US, 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24968
LENGTH: 163 ORGANISM: Pseudomonas aeruginosa

Score 38; DB 4; Length 163; Pred. No. 46; 1; Mismatches 0; Indels Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative

JS-09-252-991A-24968

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Gaps

4 RKPTCGS 10 66 RRPTCGS 72 ઠ B

US-09-252-991A-25490

GENERAL INFORMATION:
FALSE STATE OF INVENTION:
TITLE OF INVENTION:
FILS REFRENCE:
TITLE OF INVENTION:
ABPLICANT:
FILS REFRENCE:
TOTHE OF INVENTION:
FILS REPRENCE:
OURSENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR SEQ ID NOS: 33142
SEQ ID NO 25490

55.1%; Score 38; DB 4; Length 469; US-09-252-991A-25490

Query Match

ORGANISM: Pseudomonas aeruginosa

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Sequence 29509, Application US/09252991A
Sequence 29509, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
APPLICATURY: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT RILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29509
LENGTH: 269
TYPE: PRI
                                                                   Sequence 19336, Application US/09252991A
| Sequence 19336, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICATT:
| APPLICATT:
| APPLICATT:
| APPLICATT:
| APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| FILLE REFERENCE: 10.196.136
| CURRENT APPLICATION NUMBER: US/09/252,991A
| CURRENT PLING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NO. 19336
| SEQ ID NO. 19336
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APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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Pred. No. 57;
1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.6%; Score 37; DB 4; I 50.0%; Pred. No. 1.1e+02; ive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 8597, Application US/09489039A | Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 1
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Best Local Similarity 50.0
Matches 6, Conservative
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US-09-252-991A-29509
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US-09-489-039A-8597
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                                                                                                                                                                                                                                       Sequence 21585, Application US/09252991A
Sequence 21585, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21585
LENGTH: 619
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; Sequence 5920, Application US/09513999C
; Patent No. 6783961;
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumas Milne Edwards, J.Y.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REPERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-26
; PRIOR PAPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.Pm
; SEQ ID NO 5920
; LENGTH: 88
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Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
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; OTHER INFORMATION: Xaa=Pro or Thr
US-09-513-999C-5920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.1%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                              113 RKPTCSATSR 122
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                                                                              4 RKPTCGSSQR 13
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ORGANISM: Homo sapiens
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LQKPTCG 86
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                                                                                                                                                                                                                               US-09-252-991A-21585
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Length 1299;
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Patent No. 5858710;
GENERAL INFORMATION:
APPLICANT: Bandam: Olga
APPLICANT: Bandam: Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: TUMOR-ASSOCIATED KAZAL INHIBITOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREE: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 5; 1
Pred. No. 5.1e+02;
4; Mismatches 1
            Diskette, 3.50 inch, 720 Kb
                                                                            SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
PRICIATION NUMBER: PCT/US95/08354A
FILING DATE:
CLASSIFICATION DATA:
PRICR APPLICATION DATA:
PRICR APPLICATION NUMBER: 08/272,368
FILING DATE: 8 July 1994
ATTORNEY/AGENT INFORMATION:
NAME: WONGACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-203 PC
TELECOMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM. DOS
SOFTWARE: FastSEG Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,670
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0155 US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                          TELEPAN: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%;
                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.0
Matches 5; Conservative
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489 IKQPTCGSGR 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
            MEDIUM TYPE:
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PCT-US95-08354A-2
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US-08-744-670-6
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE OF INVENTION: ARCUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: US 60/074,788
PRIOR FILING DATE: US 60/074,190
PRIOR FILING DATE: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20121
LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-20121
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                                                                                                                                                                                                                                                                       53.6%; Score 37; DB 4; Length 362;
55.6%; Pred. No. 1.5e+02;
tive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Temple University - Of The APPLICANT: Commonwealth System of Higher Education TILLE OF INVENTION: JAR3 PROTEIN TYROSINE TITLE OF INVENTION: JAR3 PROTEIN TYROSINE TITLE OF INVENTION: MINASE AND DNA ENCODING THE SAME NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSEE: & Monaco, P.C. STREET: Suite 1800, Two Penn Center CITY: Philadelphia STREET: Suite 1800, Two Penn Center CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A. ZIF: 19102
CONFUTER READABLE FORM:
CURRENT APPLICATION NUMBER: US/09/489,039A;
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747;
PRIOR FILING DATE: 1999-01-29;
NUMBER OF SEQ ID NOS: 14342;
SEQ ID NO 8597
LENGTH: 362;
TYPE: PRT
CREAMING Rebsiella pneumoniae
US-09-489-039A-8597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20121, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-08354A-2; Sequence 2, Application PC/TUS9508354A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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8 AGLRRPPAGAERR 20
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168 EPTCGATER 176
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US-09-252-991A-20121
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Search completed: November 10, 2004, 15:57:19

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sequence 332, App Sequence 577, App Sequence 577, App Sequence 577, App Sequence 172364, Sequence 198430, Sequence 198429, Sequence 198429, Sequence 67911, A Sequence 67911, A Sequence 20990, Sequence 219968, Sequence 2183027, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 64, App Sequence 5183027, Sequence 5183027, Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-022-750-65

1 Sequence 65, Application US/10092750

2 Sequence 65, Application US/10092750

3 Publication No. US20030032157A1

4 Particant: Alpin, Unia

4 Particant: Alpin, Martin C.

7 ITLE REFERENCE: 50036/05002,

7 TILE REFERENCE: 50036/05002,

7 TILE REFERENCE: 50036/05002,

7 TILE REFERENCE: 2002-03-07

7 FILE REFERENCE: 2002-03-07

7 PRIOR PILLATION NUMBER: US 60/274,526

7 PRIOR PILLATION UNMBER: US 60/274,526

7 NUMBER OF SEQ ID NOS: 253

7 SOFTWARE: PastSEQ for Windows Version 4.0

7 LENGTH: 13
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6 US-10-408-765A-1557
4 US-10-707-805-332
3 US-10-707-805-377
4 US-10-707-6-622-577
4 US-10-708-845-577
5 US-10-78-845-6
5 US-10-428-115-198429
7 US-10-428-115-198429
7 US-10-428-115-198429
7 US-10-428-115-198428
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100.0%; Score 69; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-477-963-138965
US-10-477-963-138965
Sequence 138965, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SGLRKPTCGSSQR 13
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     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-65
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Sequence 138965,
Sequence 300236,
Sequence 109125,
Sequence 138962,
Sequence 332628,
Sequence 161045,
Sequence 15669,
Sequence 158860,
Sequence 256799,
Sequence 256799,
                                                                                                                                 November 11, 2004, 02:43:24; Search time 31.4128 Seconds (without alignments) 146.426 Million cell updates/sec
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1. // Caraca / Pubbaa / USO7 PUBCOMB. pep: *
2. // Caraca / Pubbaa / USO7 PUBCOMB. pep: *
3. // Caraca / Pubbaa / USO6 NEW PUB. pep: *
3. // Caraca / Pubbaa / USO6 NEW PUB. pep: *
4. // Caraca / Pubbaa / USO6 PUBCOMB. pep: *
5. // Caraca / Pubbaa / USO7 NEW PUB. pep: *
6. // Caraca / Pubbaa / USO7 NEW PUB. pep: *
7. // Caraca / Pubbaa / USO8 NEW PUB. pep: *
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10. // Caraca / Pubbaa / USO8 PUBCOMB. pep: *
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-963-138965
US-10-437-963-138965
US-10-437-963-138962
US-10-437-963-138962
US-10-437-963-138961
US-10-425-115-338616
US-10-425-115-198860
US-10-425-115-198860
US-10-425-115-198860
US-10-425-115-256799
US-10-437-963-12840
US-10-437-963-12840
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                         US-10-092-750-65
69
1 SGLRKPTCGSSQR 13
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Maximum DB seq length: 200000000
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Query
Match Length DB
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Gaps

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Score

Result

11111 12110897684321

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exercise Thomas J.
APPLICANT: Exercise Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Wei
APPLICANT: Baukharov, Andrey A.
APPLICANT: Baukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138962
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321), 963
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 109125
LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: PAT_MRT4530_13312C.1.pep
US-10-437-963-109125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 16;
Pred. No. 3.2e+02;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (1)..(323)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-138962
; Sequence 138962.
; Publication No. US2C040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-138962
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                                  TITLE OF INVENTION: Brad Mith TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER 10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138965
LENGTH: 95
TYPE.
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Sequence 300356, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
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APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: 18-12/13-220
CURRENT FILING DATE: 2003-04-28
KUNDERS OF SEQ ID NOS: 369326
SEQ ID NO 300236
LENGTH: 53
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US-10-437-963-138965
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; OTHER INFORMATION: Clone ID: MRT4577_36886C.1.pep
US-10-425-115-300236
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Pred. No. 16;
0; Mismatches 5
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
    La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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Best Local Similarity 61.5%;
Matches 8; Conservative
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ORGANISM: Zea mays
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US-10-425-115-300236
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US-10-437-963-109125
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B; CURRENT PILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENDTH: 137 TYPE: Dom
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| Sequence 45264, Application US/10425114
| Publication No. US200400348881
| General Inclusion of US200400348881
| APPLICANT: Liu, Jingdong
| APPLICANT: Zhou, Yihua
| APPLICANT: Acvalic, David K. APPLICANT: Tabaska, Jack E
| APPLICANT: Acvalic, David K. APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION NUMBER: US/10/425,114
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 73128
| SEQ ID NO 45264
| LENGTH: 245
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Sequence 198860, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICAVY: Las Rosa, Thomas J.
APPLICAVY: APPLICANY: Zhou, Yihua
APPLICANY: Consoly Yihua
APPLICANY: Consoly Yihua
APPLICANY: Consoly Yihua
APPLICANY: Consoly Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 16; Length 137;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_60266C.1.pep
US-10-437-963-161045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(137)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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US-10-425-114-45264
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Best Local Similarity 58.3%;
Matches 7; Conservative
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87 SGSRTPSCGAS 97
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ORGANISM: Zea mays
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"TILE OF INVENTION: Vibua

"TILE OF INVENTION: Plants

"TURENT APPLICATION NUMBER: US/10/425,115

"CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 31228

LENGTH: 90

TYPE ""
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US-10-45-115-338616
Sequence 338616, Application US/10425115
Sequence 338616, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Covalic, Youngwei
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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TUTLE OF INVENTION: Nucleic Acid Molecules Associated With
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Best Local Similarity 75.0%; Pred. No. 87;

Matches 6; Conservative 2; Mismatches. 0; Indels
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Pred. No. 77;
0; Mismatches 4; Indels
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; LOCATION: (1)..(103)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71985C.1.pep
US-10-425-115-338616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_47809C.1.pep
US-10-425-115-312228
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Publication No. US20040123343A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Too, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey'A.
APPLICANT: Boukharov, Andrey'A.
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Best Local Similarity 66.7%;
Matches 8; Conservative (
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55 GLRRPSCG 62
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-437-963-161045
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                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 16; Length 73
Pred. No. 5.2e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_24C.1.pep
US-10-437-963-122034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTGUKA, MOTOVUKI
APPLICANT: MAGAHARI, KENJI
APPLICANTION: NOVEL FULL-LENGTH CDNA
ITILE OF INVENTON: NOVEL FULL-LENGTH CDNA
CURRENT APPLICATION NUMBER: 00/10/094,749
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VARIES: 201-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VARIES: 201-09-14
NUMBER OF SEQ ID NOS: 3381
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122034
LENGTH: 734
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, UUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-10-408-765A-1557
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US-10-425-115-256799
; Sequence 256799, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Acvalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 17; Length 25.
Pred. No. 2.28+02;
                                                                                                                                                                                                                                                             FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_112937C.1.pep

US-10-425-115-198860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(383)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-437-963-122034

Sequence 122034, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Qu, Yongwei

APPLICANT: Wu, Wei
   FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 198860
LENGTH: 291
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Barbazuk, Brad
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                  Search completed: November 11, 2004, 07:41:45 Job time : 32.4128 secs
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-332
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APPLICANT: Sahin, Aysegul
APPLICANT: MAILS, CACAON B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, MAILS, CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REPRENCE: MRI-038
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PLING DATE: 2001-07-18
PRIOR PLING DATE: 2001-07-18
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFWMARE: PASLSCQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 1225
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                                         APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: UNDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1557
LENGTH: 1011
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Publication No. US20030124128A1
GENERAL INFORMATION:
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Wang, Youthen
Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E
Bast Jr., Robert C.
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumen
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangl
  Soumitra S.
Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-408-765A-1557
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November 10, 2004, 14:52:32; Search time 4.44128 Seconds (without alignments) 281.634 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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69
1 SGLRKPTCGSSQR 13
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summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv length: 0 length: 2000000000 sed Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: * PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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T49439 AC3412	E84213	S55205	G84708	B87553	QQBE47	B87754	S51672	OYBRC	D96581	F70080	AF3364	S25343	AB2373	JC4728
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qq	354 SGLRKP-CGSSE 364

probled chain amino acid ABC transporter, ATF-binding protein (braF-3) homolog - Archa c'Species: Archaeoglobus fulgidus
C'Species: Archaeoglobus fulgidus
C'Species: Archaeoglobus fulgidus
C'Species: Archaeoglobus fulgidus
C'Species: Archaeoglobus fulgidus
C'Species: Archaeoglobus fulgidus
C'Accession: 659369
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc. F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirhness, E.F.; Glodek, A. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
N,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.F.; Sykee, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Recession: 669369; MUID:98049343; PMID:9389475
A;Accession: 669369
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-212 <KLE>
A;Cross-references: UNIPROT:029303; GB:AECO1038; GB:AECO1032; NID:g2689361; PIDN:AAB902
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology C;Reywords: ATP-binding cassette bomology cassette proteins; ATP-binding cassette homology F;17-207/Domain: ATP-binding motif A (P-loop)

hypothetical prote

Gaps

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hypothetical protein F7J8.260 - Arabidopsis thaliana ($Species: Arabidopsis thaliana (mouse-ear cress) ($Species: Arabidopsis thaliana (mouse-ear cress) ($Species: Arabidopsis thaliana (mouse-ear cress) ($Species: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 ($Species: 07-Accession: T4596 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004 ($Species: 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #text_change 09-Jul-2004 #species 07-Feb-2000 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #species 07-Feb-2004 #specie
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Nature 408, 816-820, 2000
Apturbors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Frasch C.M.; Venter, J.C.; Davis, R.W.
A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium channel protein alpha-1 chain isoform A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Accession: All098, Also Soin 10-Soin Snutch, T.P.
R;Starr, T.V.B.; Prystay, W.; Snutch, T.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 5621-5625, 1991
A;Reference number: A41098; MUID:91288516; PMID:1648226
A;Accession: A41098
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A,Residues: 1-816 <STO>
A,Cross-references: UNIPROT:Q9SAF0; GB:AE005172; NID:g4850400; PIDN:AAD31070.1; GSPDB:G
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A; Medidues: 1-2212 (STA)
A; Residues: 1-2212 (STA)
A; Cross-references: UNIPROT: P54282; GB: M64373; NID: 9203110; PIDN: AAA40806.1; PID: 9203111
B; Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Leeter, H.A.; Davidson, N.
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A; Title: Rat brain expresses a heterogeneous family of calcium channels.
A; Reference number: A35901; MUID: 90239020; PMID: 1692134
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C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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63.6%; Pred. No. 49;
ive 2; Mismatches 2; Indels
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Pred. No. 1.1e+02;
3; Mismatches 1;
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1726 SGIQKPECGN 1735
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153 IRKASCGSSNR 163
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A; Residues: 1435-1667 <SNU>
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Best Local Similarity
Matches 6; Conserve
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Matches 7
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: C85041
C;Accession: C85041
R;Aunonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprint Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85041
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 < STO>
A;Csoretics: C;Genetics: C.STO>
A;Csoretics: C;Genetics: C.STO>
C;Genetics: C;Cenetics: C.STO>
A;Coretics: C.STO>
A;Coretic
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Cipate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
Cipate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
Cipate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
Cipate: 05-Marcherization and chromosomal mapping of the gene encoding the cellular DNA A; Reference number: A42827
A; Reference number: A42827
A; Marcherization A; Molio-92347863; PMID:1339390
A; Accession: B42827
A; Molio-1997 cills
A; Molio-1997 cills
A; Molio-1997 cills
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:109781, NCBIP:109782)
C; Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology F; 141-232/Domain: fork head DNA-binding domain homology
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Pred. No. 33;
1; Mismatches 2; Indels
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                                                                                Length 212;
                                                                                                                                                                          1; Indels
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                                                                                     DB 2;
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Pred. No. 14;
5; Mismatches
                                                                                                                             Pred. No. 5;
1; Mismatches
                                                                                     Score 43;
Pred. No.
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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AGLEKPICG 54
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A;Map position: 4
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probable ATP-binding component of ABC transporter PA3212 [imported] - Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Spaceis: Pseudomonas (Spaceis: Pseudomonas (Spaceis: Pseudomonas (Spaceis: Pseudomonas aeruginosa (Pseudomonas aeruginosa (Pseudomonas aeruginosa (Pseudomonas aeruginosa PA01, an opportunistic pat) A; Reference number: A82950; MUID:20437337; PMID:10984043 A; Astatus: Preliminary A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264 <STONA A; Residues: 1-264
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.F. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUDD:21470413; PMID:11586360
A;Accession: AC0236
A;Status: preliminary
A;Status: DNA
A;Dacidine: Lype: 
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C;Species: Yersinia pestis

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C;Accession: T47022

C;Accession: T47022

Shorteser, C; Rusnick, C; Couve, E; Frangeul, L.; Billault, A.; Kunst, F.; Carnic

Submitted to the EMBL Data Library, October 1998

A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.

A;Reference number: 224348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9HZ28; GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG066A;Experimental source: strain PAO1
C;Genetics:
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A;Residues: 1796 cKUR>
A;Cross-references: UNIPROT:Q9ZC46; GB:AL590842; PIDN:CAC90751.1; PID:g15979953; GSPDB:C;Generics:
A;Gene: YPO1936
C;Superfamily: Escherichia coli valine-pyruvate transaminase
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Pred. No. 59;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 264;
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Pred. No. 43;
1; Mismatches
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative (
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57 GLRRPTSGS 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein L7610.6 - Leishmania major
C; Species: Leishmania major
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T18316
R; Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.; Submitted to the EMBL Data Library, May 1999
A; Reference number: Z18876
A; Accession: T18316
A; Accession: T18316
A; Accession: T18316
A; Residues: 1-599 <OLI>A; Residues: 1-599 <OLI>A; Residues: 1-599 <OLI>A; Residues: 1-599 <OLI>A; Constructed to Translated from GB/EMBL, DDBJ
A; Cross-references: UNIPRCT: O97009; EMBL; AL034356; NID:e1371878; PID:e1371561; PIDN: CAAZ C; Genetics:
A; Note: L7610.6
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C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Species: Aeropyrum pernix
C'Spaces: C'O-Aug-1999 #sequence _revision 20-Aug-1999 #text_change 09-Jul-2004
C'Accession: C'2588
R'Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
BN, Kawarabayasi, Y.; Hino, Y.; Tanahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
A; Feference number: A)2450; MUD:99310339; PMID:10382966
A; Steference number: A72450; MUD:99310339; PMID:10382966
A; Steference DNA
A; Molecule type: DNA
A; Molecule type: DNA
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A, Residues: 1-109 < KAW>
A, Cross-references: UNIPROT: Q9YCT6; DDBJ: AP000061; NID: g5104821; PIDN: BAA80161.1; PID: d1
A, Experimental source: strain Kl
C, Genetics:
A, Gene: APE1176
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A;Molecule type: DNA
A;Residues: 1-460 <BEV>
A;Residues: 1-460 <BEV>
A;Crossidues: 1-460 <BEV>
A;Crossidues: UNIPROT:Q9LFA8; EMBL:AL137189
A;Crossiduental source: cultivar Columbia; BAC clone F7J8
C;Genetics:
A;Map position: 5
A;Introns: 28/2; 57/3; 398/3
A;Note: F7J8.260
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7
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Pred. No. 56;
2; Mismatches
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Pred. No. 21;
3; Mismatches
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80 SGIRRPSSSSSR 92
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Best Local Similarity 66.7
Matches 6, Conservative
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63 TGLRRPQCG 71
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Matches 7; Conserv
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Job time : 5.44128 secs
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26453; T27501
R;Lennard, N.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z20216
A;Actatus: preliminary; translated from GB/EMBL/DDBJ
A;Resperimental source: Clone Y113G7C
A;Experimental source: clone Y113G7C
R;Basham, V.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20377
A;Reference number: Z20377
A;Reference number: Z20377
A;Reference number: Z20377
A;Reference number: C20377
A;Reference nu
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 877401
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77401
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <KANA
A;Cross-references: UNIPROT:P73464; EMBL:D90906; GB:AB0001339; NID:g1652492; PIDN:BAA1750
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s1r1222
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A;Map position: 5
A;Introns: 31/2; 216/3; 279/3; 343/3; 400/3; 428/1; 450/3; 489/1; 532/3; 593/2
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                                      A;Cross-references: UNIPROT:092C46; EMBL:AL031866; PIDN:CAA21365.1
A;Experimental source: strain 6/69
C;Superfamily: Escherichia coli valine-pyruvate transaminase
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55.1%; Score 38; DB 2; Length 619;
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A, Molecule type: mRNA
A, Residues: 1-376 < Old.
A, Residues: 1-376 < Old.
A, Residues: 1-376 < Old.
A, Cross-references: UNIPROT: Q28629, GB: U26535, NID: g847787, PIDN: AAA67896.1; PID: g84778
A, Cross-references: UNIPROT: Q28629, GB: U26535, NID: g847787, PIDN: AAA67896.1; PID: g84778
C, Comment: This protein involved in leukocyte-endothelial adhesion, it mediates adhesion
C, Superfamily: L-selectin, C-type lectin homology; complement factor H repeat homology;
F, 1-37 / Domain: C-type lectin homology & LGP-
F, 18-376 / Product: L-selectin #status predicted < MAT-
F, 160-191 / Domain: EGF homology & EGF-
F, 197-254 / Domain: complement factor H repeat homology < FHR>
P, 259-316 / Domain: complement factor H repeat homology < FHR>
                                                                                                                                                                                                                                                                                                                  L-selectin precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: O4-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: JC4892
C;Accession: JC4892
R;Oian, J.; Huang, X.; Marks, R.M.
Biochem. Biophys. Res. Commun. 225, 406-412, 1996
A;Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant protein
A;Reference number: JC4892; MUID:96354800; PMID:8753776
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BAD17472
ID BAD17472
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Matches
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CSTRAIN=VC-16, DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=939475; DOI=10.1038/37052;
KIERK H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B.,
Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Dee N.H., Sutton G.G., Gill S.R.,
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
A Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
Abou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
Altuctback T.R., Cotton M.D., Sprigger T., Artiach P., Kaine B.P.,
Aykes S.M., Sadow P.W., D'Andrea K.P., Bowmann C., Fujil C.,
Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
Woese C.R., Varler J.C.,
The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-1998 (TrEMBLrel. 26, Last sanotation update)
01-NR-2004 (TrEMBLrel. 26, Last annotation update)
Branched-chain amino acid ABC transporter, ATP-binding protein (BraF-31) (Methanococus jannasch.
OrderedLocusNames=AF0959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Belseny W., Berger C., Cooke R., Grellet F., Laudie M., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
65.9%; Score 45.5; DB 2; Length 438;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133452; CAB63018.1; -.
HY5785; H45785.
HYPOCHETICAL protein.
SEQUENCE 438 AA; 47254 MW; C0402BID2F43CF0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Buryarchaeota, Archaeoglobi, Archaeoglobales,
Archaeoglobaceae; Archaeoglobus.
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EMBL, AE001038; AAB90284.1; -.
PIR, G69369; G69369.
                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F26013.180.
Name-F26013.180,
Arabidopsis thaliana (Mouse-ear cress).
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                                                                         438 AA
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                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                      Q9SCZ5;
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                          RESULT 2
Q9SCZ5
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029303
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilioppida; Poales; Poaceae;
Enthartoideae; Oryzea; Oryza; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, PAP005644; BAD17472.1; -.
Hypothetical protein.
SEQUENCE 354 AA; 38565 MW; 745AB1B003575BEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBb0056122.17.
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Last annotation update)
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                             62.3%; Score 43; DB 77.8%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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10-MAY-2004 (TrEMBLrel. 27, Last seque
110-MAY-2004 (TrEMBLrel. 27, Last annot
Hypothetical protein OSJNBb0056122.17.
OSJNBB0056122.17.
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SEQUENCE FROM N.A.
SPIGOBL L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Spigoll L.A., Mtero A., Shah R., O'Shaughnessy A., Rodriguez M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mawes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name=F4C21.18; Synonyms=AT4g03250, hd-14;
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:transcription of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR009057; Homeodomain_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K., Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N., McCombie W.R.; Suk.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Ciarbelli A.R., Carabelli M., Ruzza V., Sessa G., Steindler C.,
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STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Glora sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC clore:0SJNBD0056122.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, APPOS644; BAD17472.1; -.
Hypothetical protein.
SEQUENCE 354 AA; 38565 MW; 745AB1B003575BEA CRC64;
                                                                                                                                                                                                                             / Match 62.3%; Score 43; DB 2; Length 354; Local Similarity 70.0%; Pred. No. 32; 1; Indels nes 7; Conservative 2; Mismatches 1; Indels
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EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-I.- SUBCELLULAR LOCATION: Nuclear (By similarity).

EMBL; ACO05275; AAD14453.1; -.

EMBL; A4441296; CAD29664.1; -.

EMBL; Al161496; CAB77810.1; -.

PIR; C85041; C85041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Parnell L.D., McCombie W.R.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruberti I.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parnell L.D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      2 GLRKPTCGSS 11
                                                                                                                                                                                                                                                                                                                                                                                       33 GMRAPSCGSS 42
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SEQUENCE FROM N.A.
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Matches
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Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacee; Pseudomonas.
NCBI_TaxID=323;
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                                                                                                                                                                                                                                                                                                 60.9%; Score 42; DB 2; Length 476; 53.8%; Pred. No. 65; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00104; HOMEOBOX.
ProDOM: PD000105; HOMEOBOX.
SMART; SM00389; HOX; 1.
PROSITE; PS50071; HOMEODOX. 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SRQUENCE 476 AA; S3493 MW; D9322A290AFC4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0TN-2003 (TrEMBLrel. 24, Created)
01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Nickel ABC transporter, ATP-binding protein, putative.
OrderedLocusNames=FSPF03091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 60.9%; Score 42; DB 2;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 53...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SGLRKPTCGSSQR 13
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69 SGLRQDSCGSTKQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLEKPTCG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GLRKPTCG 9
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Q880R1
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Ouery Match
Best Local Similarity 70.0.
Tr Conservative
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les 7; Conservative
                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 MRKPTCGLCQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 MRKPTCGLCO 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LRKPICGSSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LRKPTCGSSQ 12
                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ17118
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                                                                 Q6WQJ1
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ICHY_CAIMO
                     RESULT 10
Q6WQJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSDDR
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AAQ17118
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                                                                                                                                                                                                                                                                                                                                                    Consider M. Wilson M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M., A Terao K., Sugano S., Hashimoto K.;

Terao K., Sugano S., Hashimoto K.;

Terao K., Sugano S., Hashimoto K.;

Tornomolgus monkey testicular cDNAs for discovery of novel human genes

In the human genome sequence.";

BMC Genomics 3:36-36(2002).

REMBL; ABNO7012; BAB62957.1; -.

RHSSP; Q00420; IAWC.

InterPro; IPR002110; ANK.

RPRINTS; PR01415; ANK/RIN.

RAMART; SM00248; ANK, S.

RR PROSITE; PS50089; ANK, S.

RR PROSITE; PS50089; ANK, S.

RR ANK repeat; Hypothetical protein.

Q SEQUENCE 733 AA; 81674 MW; OD4E69C1B8E025AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drassica napus (Rape).
Brussica napus (Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Endear Sescicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Butelecstomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.9%; Score 42; DB 2; Length 733; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERGIN=canola;
Gao Y.P., Gusta L.V.;
Gao Y.P., Gusta L.V.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139818; AAD38621.1; -1.
Interpro; IFFR002628; PSII_MSP.
Pfam; PF01716; MSP; 1.
SEQUENCE 274 AA; 29642 MW; 357A3E621FF41A0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSKE68,
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
33 kDa oxygen evolving protein of photosystem II.
                                             733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AA.
                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 SGLLSPVCGSMQ 341
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SGLRKPTCGSSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RKPTCGSSQR 13
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Testis:
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Q9XH68
RESULT 8
                     095K15
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205 RRPTCASSSR 214

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STRAN=CSPEL/65,
Horiquchi S., Tashiro K., Takahashi J., Hashimoto N., Nakano I.,
Tsuchida Y., Hirai H., Honjo T.; Tsuchida Y., Hirai H., Honjo T.;
Tsuchida Y., Hirai H., Honjo T.;
"NSDDR a novel tetra-spanning transmembrane protein with a unique integration pattern to the plasma membrane regulates the extension of the dendritic trees of Purkinje cells.";
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
ENBL; AY275376; AAQ17118.1; -. EEMBL, REAC2349D4E3503E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CSTBL/6J;
STRAIN=CSTBL/6J;
Foriguchl S., Tanhiro K., Takahashi J., Hashimoto N., Nakano I., Teuchida Y., Hirai H., Honjo T.,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY275376, AAQ17181.;
InterPro; IPR002921; Lipses J.
InterPro; IPR00262; Lipses AS.
Fran, PP01764; Lipses AS.
Fran, PP01764; Lipses AS.
SROUENCE 1044 AA, 115375 WW; E2AC2349D4E3503E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.4%; Score 41; DB 2; Length 104
70.0%; Pred. No. 2.2e+02;
tive 1; Mismatches 2; Indels
                           Q6WQJ1;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Neural stem cell-derived dendrite regulator.
Name=NSddr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Neural stem call-derived dendrite regulator.
PRT; 1044 AA.
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PROSITE; PS00028; ZĪNC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
PROSITE; PS50463; ZNZ_CY6_FUNGAL_1; UNKNOWN_1.
PROSITE; PS50048; ZNZ_CY6_FUNGAL_2; 1.
DNA-binding; Metal-binding; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUTA LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BX224012; CAD70758.1; -.
HSSP; P07248; 2ADR.
GO; GO:0005634; Cincleus; IEA.
GO; GO:0005634; Cincleus; IEA.
GO; GO:000557; Firanscription factor activity; IEA.
GO; GO:0006357; Firanscription of transcription, DNA-dependent; IEA.
InterPro; IPR00138; Fungi Trscrp_N.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00172; Zn c1H2; Z.
Pfam; PF00172; Zn c1H2; Z.
PRINTS; PR00054; FUNGALZNCYS.
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01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-MAR-2004 (TrEWBLrel. 26, Last annotation update)
DMRTI protein.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B.
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 AA; 35330 MW; 91E67B69213E9E9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 AA
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     Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Related to transcriptional activator CMR1
Name=80A10.010;
                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%;
60.0%;
  77.8%;
                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00066; GAL4; 1.
SMART; SM00355; ZnF C2H2; 2
     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 60.0
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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91 OKPTCGACOK 100
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                                                                                        2 GLRKPTCGS
                                                                                                                                          18 GLAKPACGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             "Kazal-type chymotrypsin inhibitor from duck pancreas.";

Comp. Biochem. Physiol. 131B:499-507(2002).

-!- FUNCTION: Inhibits chymotrypsin.

-!- SUBJUIT: Monomer.

-!- SUBJUIT: MONOMER.

-!- SUBJUIT: MONOMER.

-!- MASS SPECTROMETRY: MW=7190.9; MW_ERR=2; METHOD=MALDI; RANGE=1-65;
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MEDLINE=22423065; PubWed=12534468;
Greated A., Lambertson L., Williams P.A., Thomas C.M.;
Groated A., Lambertson L., Williams P.A., Thomas C.M.;
"Complete sequence of the IncP-9 TOL plasmid pWW0 from Pseudomonas putida.";
Environ. Microbiol. 4.856-871 (2002).
ENBL; AJ344068; CAC86687.1; --
Hypothetical protein; Plasmid.
SEQUENCE 117 AA; 12700 WW; 22CBAGEEC067638D CRC64;
                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Chymotrypsin inhibitor (DPCI).
Chymotrypsin inhibitor (DPCI).
Edairina moschata (Muscovy duck).
Edkaryota; Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cairina.
                                                                                                                                                                                                                                                                                                                                   TISSUE=Pancreas;
MEDLINE=21956294; PubMed=11959032;
Wilimowska-Pelc A., Olichwier Z., Mazurkiewicz A., Kowalska J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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By similarity.
By similarity.
Reactive bond (By similarity).
360AA7FlAA515D47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 20;
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DOMAIN 11 62 Kazal-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                        SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE-Ref.1.

-1- SIMILARITY: Contains 1 Kazal-like domain.
HSSP, PRO095; 1HPT.
INTERPRO; IPR0012350; Prot inh Kazal.
INTERPRO; IPR001239; Prot_inh Kazal-m.
Pfam; PR001290; Kazal, 1.
PRINTS; PR001290; KAZALINHBTR.
SMART; SM01280; KAZALI, 1.
PROSITE; PS001280; KAZALi, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1
Pred. No. 20;
2; Mismatches
        65 AA
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        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-Mar-2002 (TrEMBLrel. 20, C. 01-MR-2002 (TrEMBLrel. 20, Le 01-OCT-2003 (TrEMBLrel. 25, Le Hypothetical protein. Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.0%;
66.7%;
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     STANDARD;
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6 NGLRRPVCG 14
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Search completed: November 10, 2004, 15:53:24 Job time: 23.867 secs

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Best Local Similarity 42.9
Matches 12, Conservative
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US-09-537-357-11
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                                                                                                                     November 10, 2004, 14:55:47; Search time 11.5658 Seconds (without alignments) 143.349 Million cell updates/sec
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1 AGTQPLILAQFMRVGGDELLHFLLW 25
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| Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application: Tribe of Sequence 2772, Application: Tribe of INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: ARGUST OF 1980 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27772 | Sequence 27
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Sequence 2, Appli
Sequence 2823, Ap
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Sequence 22239, A
Sequence 7532, Ap
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Sequence 11996, A
Sequence 11898, A
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Sequence 19064, A
Sequence 19064, A
Sequence 2066, A
Sequence 2066, A
Sequence 2069, A
Sequence 2955, Appl
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2052, Ap
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US-09-252-991A-28693
US-09-252-991A-228693
US-09-252-991A-22239
US-09-543-681A-7532
US-09-543-681A-7532
US-09-983-110-4674
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US-09-252-991A-13999
US-09-252-991A-13999
US-09-252-991A-13999
US-09-252-991A-31999
US-09-252-991A-31999
US-09-252-991A-31999
US-09-252-991A-3699
US-09-252-991A-3699
US-08-252-991A-32699
US-08-252-991A-32699
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Fatent No. 6271018
GENERAL INFORMATION
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: NUSKMELON (CUCUMIS MELO) HYE;
TITLE OF INVENTION: LYASE AND USES THEREOF
TITLE REFRENCE: 06027.0002
CURRENT PILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1:
LENGTH: 62
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; ORGANISM: Capsicum annum (green pepper)
US-09-537-357-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27772
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Application US/10042991

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Sequence 25,
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                                                           Gaps
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ian M. Whitehead
APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERRNCE: 06027.0001
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 25
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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Patent No. 6271018

GENERAL INFORMATION:
TITLE OF INVENTION: MATHALIE Trijet

TITLE OF INVENTION: MUSEMELON (CUCUMIS MELO) HYDROPEROXIDE

TITLE OF INVENTION: LYASE AND USES THEREOF

FILE REFERENCE: 06027.0002

CURRENT FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
37.9%; Score 50; DB 3; Length 480;
Best Local Similarity 31.6%; Pred. No. 5.6;
Matches 12; Conservative 5; Mismatches 7; Indels
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37.9%; Score 50; DB 3; Length 480;
Best Local Similarity 31.6%; Pred. No. 5.6;
Matches 12; Conservative 5; Mismatches 7; Indels
              37.9%; Score 50; DB 3; Length 62; 31.6%; Pred. No. 0.53; ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 GYQPLVMKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 GYQPLVWKDPKVFDEPEKFMLERFTKEKGKELLINYLFW 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GTQPLI------LAQFMRVGGDELLHFLLW 25
                                                                                                                       6 GYQPLVMKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 43
                                                                                                  -LAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Capsicum annum (green pepper)
US-09-078-173A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Capsicum annum (green pepper)
US-09-537-357-32
                                                                                                                                                                                                  RESULT 3
US-03-078-173A-25
; Sequence 25, Application US/09078173A
; Patent No. 6200794
                 Query Match 37.9
Best Local Similarity 31.6
Matches 12, Conservative
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RESULT 5 US-10-042-991-25

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Sequence 2795, Application US/09583110

Sequence 2795, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
PAPLICANTION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;
TITLE OF INVENTION: Pneumoniae for Diagnostics, and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics, and Therapeutics
TITLE OF INVENTION: NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR PILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-10

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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Unacan Gaskin
APPLICANT: Unacan Gaskin
APPLICANT: Unacan Gaskin
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: UNASER AND USES THEREOF
TITLE OF INVENTION: 2002-01-09
CURRENT FAPLICANTION NUMBER: US/10/042,991
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 27
NUMBER: FastSEQ for Windows Version 3.0
IENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
37.9%; Score 50; DB 4; Length 480;
Best Local Similarity 31.6%; Pred. No. 5.6;
Matches 12; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GIQPLI------LAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ; ORGANISM: Capsicum annum (green pepper) US-10-042-991-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-46059
; Sequence 46059, Application US/09270767
; Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 FMRVGGDELLHFLLW 25
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Best Local Similarity
Matches 8; Conserv
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US-09-583-110-2795
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UG-09-398-239-5

Sequence 5, Application US/09398239

Patent No. 6407216

GENERAL INFORMATION:
APPLICANT: Bosanthal, Arnon
APPLICANT: Stone, Domna
TITLE REFERENCE: P105001

CURRENT APPLICATION Vertebrate Smoothened Proteins
FILE REPERENCE: P105001

CURRENT FILING DATE: 1999-09-20

EARLIER APPLICATION NUMBER: US/09/398,239

CURRENT FILING DATE: 1996-09-20

EARLIER FILING DATE: 1996-09-30

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 5
                            Vertebrate Smoothened Proteins
                                                                                                                         CITAGE: 1 DAW WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/953,823A
FILING DATE: 30-Sep-1997
CLASSIFICATION NUMBER: 60/02707
FILING DATE: 30-Sep-1997
ATTOMEY AGENT INFORMATION:
NAME: SYODOGA, CTA19 G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 1950RI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 29;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-398-239-5
  APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 43.5
Matches 10; Conservative
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TYPE: Amino Acid
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                                                                                                                                                                           Score 48; DB 4; Length 219;
Pred. No. 4.8;
                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bosauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothened Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSED: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGAM, CRAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/525-1489
TELEPHONE: 650/525-1489
TELEPHONE: 650/525-1489
TELEPHONE: G50/525-1489
SEQUENCE CHARACTERISTICS:
LONDYH: 1036 amino acids
                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTOPLILAOFMRVGGDELLHFL 23
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-720-484A-5; Sequence 5, Application US/08720484A; Patent No. 5990281; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %308-953-823A-5
% Sequence 5, Application US/08953823A
% Patent No. 6136958
% GENERAL INFORMATION:
APPLICANT: Bosauvage, Frederic
% APPLICANT: Rosenthal, Arnon
                                                                                                                                                                                                                                                                                             4 QPLILAQFMRVGGDELLHFL 23
                                                                                                           ORGANISM: Drosophila melanogaster
US-09-270-767-46059
                                                                                                                                                                           Similarity 45.0%;
9; Conservative
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46059
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.4%; Score 48; DB 4; Length 1036; Best Local Similarity 43.5%; Pred. No. 29; Matches 10; Conservative 4; Mismatches 9; Indels
                         sequence 5, Application US/09560876A; Patent No. 6492139; GENERAL INFORMATION:
APPLICANT: APPLICANT: Rosenthal, Arnon, APPLICANT: Rosenthal, Arnon, TITLE OF INVENTION: Vertebrate Smoothened Proteins; FILE REFERENCE: P105081D1; CURRENT FILING DATE: 2002-05-22; PRIOR APPLICATION NUMBER: US 60/027,070; PRIOR APPLICATION NUMBER: US 60/027,070; PRIOR APPLICATION NUMBER: US 60/027,070; PRIOR PILING DATE: 1996-09-30; PRIOR FILING DATE: 1997-09-30; NUMBER OF SEQ ID NOS: 6; LEWARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09560876A; Batent No. 6492139; GENERAL INPORMATION:
APPLICANT: de Sauvage, Frederic; APPLICANT: Rosenthal, Arnon; APPLICANT: Rosenthal, Arnon; TITLE OF INVENTION: Vertebrate Smoothened Proteins; FILE REFERENCE: P1050R1D1; CURRENT APPLICATION WUMBER: US/09/560,876A; CURRENT PPLICATION WUMBER: US 00/027,070; PRIOR FILING DATE: 2002-05-22; PRIOR FILING DATE: 1996-09-30; PRIOR FILING DATE: 1997-09-30; PRIOR FILING DATE: 1997-09-30; PRIOR FILING DATE: 1997-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: unknown amino acid US-09-560-876A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              788 AGLDPSILNEFLOKNGDFIFPFL 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    817 AGLDPSILNEFLQXNGDFIFPFL 839
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ORGANISM: Drosophila melanogaster
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NAME/KEY: unsure
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US-09-560-876A-6
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LENGTH: 1065
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TYPE: PRT
RESULT 11
US-09-560-876A-5
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RESULT 13 US-09-252-991A-18920 ; Sequence 18920, Application US/09252991A

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RESULT 14
US-09-252-991A-19103
is Sequence 19103, Application US/09252991A
is Sequence 19103, Application US/09252991A
is Patent No. 6551795
igeneral information:
if The Communication of the Application 
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ACEUGINGS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 05 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190
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Pred. No. 21;
Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 ÓPLVAQPRDPLREEAQRQRVGGGELQHLAL 225
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; Sequence 26648.
Patent No. 6551795
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18920
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Best Local Similarity 43.3%;
Matches 13; Conservative
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Best Local Similarity 52.61
Matches 10; Conservative
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Search completed: November 10, 2004, 15:57:20 Job time : 12.5658 secs

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Sequence 214, App Sequence 236063, Sequence 236063, Sequence 246400, A Sequence 17358, Sequence 177358, Sequence 177359, Sequence 144679, Sequence 144680, Sequence 147272, Sequence 147272, Sequence 147272, Sequence 204013, Sequence 204013, Sequence 204013, Sequence 204013, Sequence 204013, Sequence 219262,
145, App 3353, Ap 4, Appli 174116,

Sequence 1 Sequence 5 Sequence 1

Sequence Sequence

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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VESCULO 192-750-66

1 Sequence 66, Application US/10092750

2 Publication No. US20030032157A1

2 PUBLICANT: NPORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

TILE OF INVENTION: Polyeptides Interactive with BCL-XI

FILE REFERENCE: 50036/050002,

CURRENT FILING DATE: 2002-03-07

PRIOR PAPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 66

LENGTH: 25

TYPE: PRI

CREANTION: Homo sapiens

US-10-092-750-66
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                                    US-10-282-123A-77667
US-10-424-599-236663
US-10-425-114-46400
US-10-425-114-46400
US-10-425-114-73004
US-10-425-114-73004
US-10-437-963-17358
US-10-437-963-144679
US-10-369-493-14329
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US-10-282-122A-60085
US-10-767-701-50265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-425-115-229512
; Sequence 229512, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Sequence 229512,
Sequence 48127, A
Sequence 40985, A
Sequence 11, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 53335, A
Sequence 53315, A
Sequence 65315, A
Sequence 67552, A
Sequence 67552, A
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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5 US-10-425-115-229512
5 US-10-425-114-40985
10S-10-425-114-40985
7 US-09-884-206A-11
7 US-09-884-206A-12
8 US-10-425-115-327061
8 US-10-425-115-3219
10S-09-884-206A-32
10S-09-884-206A-32
10S-09-884-206A-32
10S-09-884-206A-32
10S-10-425-114-53219
10S-10-425-114-67552
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132
1 AGTQPLILAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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Match Length
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Gaps

ö 25;

Score

Result No.

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Gaps

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Length 163;

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Page 2

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5)313)B

CURRENT APPLICATION NUMBER: 105/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 40985

LENGTH: 163

TYPE: ...
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APPLICANT: Experisor, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TTIE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 2003-04-28
CURRENT APPLICATION UNDER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09884260A

Sequence 11, Application US/09884260A

Ratent No. US20202098570A1

GENERAL INFORMATION:

APPLICANT: Alan Brash

APPLICANT: Nathalier Tijet

TITLE OF INVENTION: MYSKMELON (CUCUMIS MELO) HYDROPEROXIDE

TITLE OF INVENTION: LYASE AND USES THEREOF

FILE REFERENCE: 06027.000202

CURRENT APPLICATION NUMBER: US/09/884,260A

CURRENT FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US/09/537,357

PRIOR PRICATION NUMBER: 099/537,357

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GTOPLI------LAOFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GYQPLVWKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: LIB3059-042-B9_FLI.pep
US-10-425-114-40985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.6%; Score 51; DB 15; Best Local Similarity 50.0%; Pred. No. 5.9; Matches 10; Conservative 5; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Capsicum annum (green pepper)
US-09-884-260A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 327061, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTOPLILAOFWRVGGDELL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 AGLEPLIKARFGRLAGGDLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-425-115-327061
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US-09-884-260A-11
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       . APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

ITTLE OF INVENTION: Plants

FILE REPRENENCE: 38-21(53-22)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 229512

LENGTH: 168

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.6%; Score 51; DB 15; Length 161; Best Local Similarity 50.0%; Pred. No. 5.8; Matches 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: LIB3279-043-H12_FLI.pep
US-10-425-114-48127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), OTHER INFORMATION: Clone ID: MRT4577_140909C.1.pep
US-10-425-115-229512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/FEXY: unsure
COCTION: (1)..(168)
OTHER INFORWATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGTOPLILAOFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-425-114-40985
; Sequence 40985, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTQPLILAQFMRVGGDELL 20
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22 AGLEPLLKARFGRLAGGDLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-425-114-48127
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Gaps

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US-10-757-701-55335
US-10-767-701-55335
US-10-767-701-55335
Sequence 55335, Application US/10767701
Sequence 55335, Application US/20040172684A1
Sequence 55335, David K.
Publication No. US2004017084
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Applicant Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53355)
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 55335
LENGTH: 103
                                                                                                                                                                                                                     APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Alan Susarenko
APPLICANT: Duncan Gaskin
APPLICANT: Duncan Gaskin
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (FSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: GLOZ7.0001U3
TITLE OF INVENTION: 10027.0001U3
FILE REFERENCE: 06027.0001U3
CURRENT APPLICATION NUMBER: US/10/042,991
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.9%; Score 50; DB 13; Length 480; Best Local Similarity 31.6%; Pred. No. 28; Matches 7; Indels 1
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Pred. No. 11;
1; Mismatches 8; Indels
     389 GYQPLVMKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 426
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LOCATION: (1)..(103)
OTHER INFORMATION: unsure at all Xaa locations
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; OTHER INFORMATION: Clone ID: 30161891.pep
US-10-767-701-55335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Capsicum annum (green pepper)
US-10-042-991-25
                                                                                                     RESULT 9
US-10-042-991-25
Sequence 25, Application US/10042991
Publication No. US20020142407A1
GENERAL INFORMATION:
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Best Local Similarity 55.0%;
Matches 11; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-114-53219
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Publication No. US20040088752A1
GENERAL INFORMATION
APPLICANT: Howe, Gregg
APPLICANT: Itch, Aya
TITLE OF INVENTION: Divinyl Ether Synthase Gene, Protein, and Uses Thereof
FILE REFERENCE: MSU-06815.
CURRENT APPLICATION NUMBER: US/10/381,870
PLICA PELICATION NUMBER: 60/238,415
PRIOR FILING DATE: 2003-11-17
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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Sequence 32, Application US/09884260A

Fatent No. US20202098570A1

GENERAL INFORMATION:

APPLICANT: Alan Brash

TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE

TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE

TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO)

FILE REFERENCE: 06027.000202

CURRENT APPLICATION NUMBER: US/09/884,260A

CURRENT FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: 096-19

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.9%; Score 50; DB 15; Length 476; Best Local Similarity 31.6%; Pred. No. 28; Matches 12; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                            Query Match

37.9%; Score 50; DB 17; Length 70;
Best Local Similarity 47.1%; Pred. No. 3.4;
Matches 8; Conservative 5; Mismatches 4; Indels
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37.9%; Score 50; DB 9; Length 480;
Best Local Similarity 31.6%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 GYOPLVMKDPKVFDEPEKFVLERFTKEKGKELLNYLFW 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GTOPL-----ILAOFMRVGGDELLHFLLW 25
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                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6134C.1.pep
US-10-425-115-327061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Capsicum annum (green pepper)
US-09-884-260A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Lycopersicon esculentum US-10-381-870-5
                                                                                                                                                                                                                                                                                                                       23 ASVQPVLIQQYMSVGGE 39
                                                                                                                                                                                                                                                                                         1 AGTOPLILAOFMRVGGD 17
LENGTH: 70
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GTQPLI-
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LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-381-870-5
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APPLICANT: Shen, Let
APPLICANT: Shankets, Richard A.
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APPLICANT: Shankets, Richard A.
APPLICANT: Spaderna, Seveen K.
APPLICANT: Spaderna, Seveen K.
APPLICANT: Spaderna, Seveen K.
APPLICANT: Taupier, Bayan D.
APPLICANT: Techernev, Velizar T.
APPLICANT: Voss, Edward S.
APPLICANT: APPLICANT: Voss, Edward S.
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Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tohernev, Vellzar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
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Padigaru, Muralidhara
                                                    Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
Lepley, Denise M.
Liu, Kiaohong
                                                                                                                                                                                                                                                                                                                     Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                    , Luca
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Sequence 67552, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Screen, Screen, Screen, Screen, Screen, Screen, Story E
APPLICANT: Cao, Yongwei
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Paparicanton: Nucleic Acid Molecules and Other Molecules Associated With
TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
Sequence 53219, Application US/10425114
Publication No. US2004003488BA1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jinddong
APPLICANT: Enou, Yihua
APPLICANT: Screen, Serven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Solven E
APPLICANT: Nouse and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
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US-10-425-114-67552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: 700242574_FLI.pep
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Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John P. II
APPLICANT: Boldog, Ferenc L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTOPLILAOFMRVGGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AKVQPVLIQQYMSVGGE 27
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LENGTH: 276
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LENGTH: 287
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us-10-092-750-66.rapb
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APPLICANT Taugher, Kaymond T
APPLICANT Taugher, Kaymond T
APPLICANT Taugher, William M
APPLICANT Gross, William M
APPLICANT Sterkers, Edward S
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT Sherine E
APPLICANT PAGGARU, MURALIdhara
APPLICANT PAGGARU, MURALIGHARA
APPLICANT PAGGARU, 2002-06-18
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
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36.4%; Score 48; DB 15; Length 2447;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 12; Conservative 3; Mismatches 5; Indels ;
                                      Zerbusen, Bryan
Patturajan, Meera
Taupier, Raymond T
Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Takifugu rubripes
US-10-369-072-28
Spytek, Kimberly
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2; Gaps

ð g RESULT 15
US-10-306-762-214

i Sequence 214, Application US/10306762

j Publication No. US203018722041

j GENERAL INFORMATION:
 APPLICANT: Park, Frances
 APPLICANT: Buchana, Sean Grant
 APPLICANT: Buchana, Sean Grant
 APPLICANT: Buchana, Sean Grant
 APPLICANT: Buchana, Sean Grant
 TILLE OF INVENTION: MCABAL
 TILLE OF INVENTION: MONONUCLECTIDE BINDING PROTEIN (FNNBP)
 TILLE REPRENCE: 52498-20011.00
 CURRENT PILICATION NUMBER: US/10/306,762
 CURRENT FILLING DATE: 2003-04-16
 PRIOR APPLICATION NUMBER: US 60/334,132
 NUMBER OF SEQ ID NOS: 242
 SOFTWARE: FastSEQ for Windows Version 4.0

seq ID NO 214

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;
                                                                                         Query Match 35.6%; Score 47; DB 14; Length 315; Best Local Similarity 50.0%; Pred. No. 53; Matches 8; Conservative 4; Mismatches 4; Indels
; LENGTH: 315
; TYPE: PRT
; OKGANISM: D hafniense (23116726)
US-10-306-762-214
                                                                                                                                                                           2 GTQPLILAQEMRVGGD 17
|::|:|||||||||||||62 GSEPALLAQAARIGAD 77
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Search completed: November 11, 2004, 07:41:45 Job time : 60.4093 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 14:50:40 ; Search time 41.9039 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

Title: US-10-092-750-66
Perfect score: 132
Sequence: 1 AGTQPLILAQFMRVGGDELLHFLLW 25

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	escription	•	ycobact	9		Q9arh8 lycopersico	Q9xgi8 lycopersico		Q9arh7 capsicum an	Q93yf8 nicotiana a	_				۰.	O85168 pseudomonas	•	_	_	plasmid	plasmid	solanuu	trus	citrus	citrus j		Cad79441 suberites	suberi	6glq4 xenopus	91682	a9 droso	13149
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073YV9 PRELIMINARY; PRT; 456 AA. 073YV9; 05-JUL-2004 (TEMBLrel. 27, Created) 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

PRELIMINARY;

RESULT 2 Q73YV9 ID Q73YY AC Q73YY DT 05-JI

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Q25542 nereis dive Q25542 nereis dive Q6bm19 debaryomyce Q9rv87 deinococcus Q8vk1 lactobacill Q9kvk1 vibrio chol Q8pg03 xanthomonas Q8yq1 bradyrhizob Q73m3 thermus the Q72gm3 thermus the Aas82167 thermus the Q896q1 clostridium Q8zxm2 pyrobaculum Q7cw29 agrobacteri
75 75
Q25542 Q8HT81 Q6HT81 Q6ENL9 Q5RVR1 Q8 BVK1 Q8 BVK1 Q8 PGG3 Q7 STE4 Q7 SCG3 Q7 SCG3 Q7 SCG3 Q7 SCG3 Q7 SCG3 Q8 SCG1 Q8 SCK0 Q8 SCK0 Q8 SCK0 Q7 CWZ9
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PRT;  Created) Last and Comyces of the properties  a_like MW;	Sco Pre 2;	
1 10 10 10 10 10 10 10 10 10 10 10 10 10	Lambda PCI. 1. 10156	38.6%; Similarity 50.0%; 9; Conservative
OFFX21  OFFX21  OFFX21  OS-UTL-2004 (TEMBLE)  OS-UTL-2004 (TEMBLE)  SIMILAR to SP P38249 S  CARNAMAS=CAGLOMO18049;  CARNAMAS=CAGLOMO18049;  CARNAMAS=CAGLOMO18049;  CARNAMAS=CAGLOMO18049;  CACHATOMYCETAIES; MIL  [1]  SCCHAROMOSE FROM N.A.  STRAIN=CBS138;  GENOLEVURES;  RADRON N.A.  STRAIN SPARMAN  SALONAMAN  SPARMAN  SALONAMAN  SPARMAN  SPARMAN  SPARMAN  SALONAMAN  NIKOLAR S.  SOUCHER S.  NICAMAN  WINCKER P., SOUCIET J.  MICKER P., SOUCIET J.  M	InterPro; IPR010982; InterPro; IPR000717; SMART; SM00088; PINT; SEQUENCE 951 AA; 1	Query Match Best Local Sim Matches 9;
RESULT O	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	QME

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                     Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solamales, Solamaceae, Solanum.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDITURE 2031213; MEDITURE 20317213; PubMed=10859201; Howe G.A., Lich A., Li L., DeRocher A.E.; Howe G.A., Tech G.I., metabolism of oxylipins in tomato. Cloning and expression of allene oxide synthase and fatty acid hydroperoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard S., Atwal A.S.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ANO28373; AAKZ1265.1;
PIR; JC7304; JC7304.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:001882; F:monooxygenase activity; IEA.
GO; GO:000118; P:electron transport; IEA.
InterPro; IPR001283; Cytochrome_P450.
InterPro; IPR001283; EP450IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 50; DB 2; Length 476; 31.6%; Pred. No. 39; 7; Indels ive 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                           -1- SIMÍÍARITY: Belongs to the cytochrome P450 family.
EMBL; AF230372; AAF67142.1; -. PIR; JC7304; JC7304.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acid hydroperoxide lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 25, Last annotation update)
Fatty acid hydroperoxide lyase.
Lycopersicon esculentum (Tomato).
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GO; GO:0004497; F:monoxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002403; EP4501V.
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                                                                                                                                                                                                                                                                                                                              lyase.";
Plant Physiol. 123:711-724(2000).
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Best Local Similarity 31.6%
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PRINTS; PR00465; EP450IV.
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01-JUN-2001
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Q9ARH8
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                                                                                                                                                                                                 Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-! COFACTOR: FAD (By similarity).
-!- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017233; AASO4161.1; -
SEQUENCE 456 AA; 48736 MW; B36BB27F78C2451E CRC64;
                                                  Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacterium; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                  Query Match
37.9%; Score 50; DB 2; Length 456;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 10; Conservative 6; Mismatches 8; Indels
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AASO4161;
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                    Name=1pd; OrderedLocusNames=MAP1844c;
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                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                         NCBI_TaxID=1770;
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LPD OR MAP1844C.
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Matches

RESULT 3 AAS04161

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Gaps

14;

476 AA; 53480 MW; 4A56DDB8131FB1C1 CRC64; Heme; Lyase. SEQUENCE 4

RESULT 4 O9LLA9

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SEQUENCE FROM N.A.
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SEQUENCE
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Shedurick B.,
Thesis (1999), University of Guelph, Dept. of Molecular Biology and
Thesis (1999), University of Guelph, Dept. of Molecular Biology and
C. -i- SiMilakulty: Belongs to the cytochrome P450 family.
DR EMBL; AJ339065; CAB43022.1; -.
DR PIR; JG7304, U73304, U73304
DR GO; GO:0016829; F:1yase activity; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:monooxygenase activity; IEA.
DR GO; GO:0006118; P:monooxygenase activity; IEA.
DR HO: CO:0006118; P:monooxygenase activity; IEA.
DR HINEPRO; IPR001128; Cytochrome_P450.
DR HinerPro; IPR001403; EP450IV.
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Bukaryota, Viridijalarae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids; Solanales; Solanaceae; Capsicum.
NCBI_TaxID=4072;
                                                Gaps
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      Length 476;
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                                            7; Indels
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TISSUE=Fruits;

Matsul K., Shibhtani M., Kajiwara T., Hase T.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; U51674; AAA97465.1;
-CO, GO:0016829; F:lyase activity; IEA.
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                                                                                                                 385 GYQPLVMKDPKVFDEPEKFVLERFTKEKGKELLNYLFW 422
                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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    Score 50; DB 2;
Pred. No. 39;
5; Mismatches
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01-NOV-1999 (TEMBLrel. 12, Last
01-CCT-2003 (TrEMBLrel. 5, Last
Hydroperoxide lyase (Fragment).
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Query Match
Best Local Similarity 31.6%;
Matches 12; Conservative
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Patty acid, Matcherostica 144, mast annotation update)
Capsicum annuum (Bell pepper).
Eukaryota; Viridiplantse; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Capsicum.
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Bukaryoca, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=49451;
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Pred. No. 40;
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                                                                                                                                                   480 AA; 54056 MW; 84A2F646A55D46C9 CRC64;
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                                                                                                                                                                                                                                                                                                         389 GYQPLVMKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 426
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last sequence update)
Last annotation update)
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GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003403; EP450IV.
PRINTS; PR00465; EP450IV.
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31.6%; Pred. No. *v,
... 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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MEDLINE=98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shiauya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii Off3.";
DNA Res. 5:55-76(1998)
BRB: Aptono002; BAA29648.1; -.
BRB: Apono002; BAA29648.1; -.
BRB: Apono002; Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
RO; GO:0016020; Papothetical protein.
Romplete proteome; Hypothetical protein.
ROSEQUENCE 573 AA; 64304 WW; 91C98EGBEF4SCC36 CRC64;
                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE=22480955; PubMed=12593519;
Packila M., Guilfoile P.G.;
"Mating, male Ixodes scapularis express several genes including those with sequence similarity to immunoglobulin-binding proteins and metalloproteases.", And the sequence similarity to immunoglobulin-binding proteins and metalloproteases."
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
NCBL_TaxID=6945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.1%; Score 49; DB 2; Length 216; 55.6%; Pred. No. 25; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Packila M., Guilfoile P.G.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY234848; AAO85921.1; -.
SEQUENCE 216 AA; 23990 MW; C9C97E9B331FE0AE CRC64;
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Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequen-MRA-2004 (TrEMBLrel. 26, Last anning prothetical protein PH0559.
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                               Exp. Appl. Acarol. 27:151-160(2002).
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Matches 10; Conservative
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STRAIN=OT3;
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NCBI_TaxID=53953;
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Best Local S:
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                      Siegler J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
L. Submitted (SEP-2001) to the cytochrome P450 family.
R. GO; O:0:0:16829; B:19xes activity; IEA.
R. GO; GO:0:0:0:4937; F:monooxygenase activity; IEA.
R. GO; GO:0:0:0:18; P:monooxygenase activity; IEA.
R. GO; GO:0:0:0:18; P:monooxygenase activity; IEA.
R. InterPro; IPR001128; Cytochrome_P450.
R. InterPro; IPR001403; E9450IV.
R. Pfam; PF00067; P450; 1.
R. PRINTS; PR00465; EP450IV.
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37.1%; Score 49; DB 2; Length 188;
Best Local Similarity 47.4%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 8; Indels
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                                                                              to the EMBL/GenBank/DDBJ databases.
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Complete proteome; Hypothetical protein.
SEQUENCE 188 AA; 21276 MW; 34C149E49889435C CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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Rhodopirellula baltica.
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                                                       Keinaenen M.;
Submitted (OCT-2001)
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Q868N1
ID Q868N
AC Q868N
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DE IS4.
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SEQUENCE FROM N.A.
STRAIN-BA71V;
MEDLINE-93281390; PubMed=8506138;
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MEDLINE=94243035; PubMed=8186465;
Gibbons B.H., Asai D.J., Tang W.J., Hays T.S., Gibbons I.R.;
"Phylogeny and expression of axonemal and cytoplasmic dynein genes in
sea urchins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and evolutionary relationships of African swine fever virus
                                                                     Tripneustes gratilla (Hawaian sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blasco R., Lopez-Otin C., Munoz M., Bockamp E.-O.O., Simon-Mateo C., Vinuela E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lopez-Otin C., Freije J.M.P., Parra F., Mendez E., Vinuela E.; "Mapping and sequence of the gene coding for protein p72, the major capsid protein of African swine fever virus.";
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Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
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1078 Aa; 121418 MW; 049AE4EA66316329 CRC64;
                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last sannotation update)
Dynein heavy chain isotype SA (EC 3.6.1.3) (Fragment).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                            uncoupled; IEA.
  PRT; 1078 AA.
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GO; GO:0042624; F:ATP binding; IEA.
GO; GO:0016787; F:ATPase activity, uncoupl
GO; GO:0000166; F:Nuclease activity; IEA.
InterPro; IPR03593; AAA_ATPase.
SMART; SM00382; AAA, 3.
ATP-binding; Hydrolase.
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MEDLINE=90223993; PubMed=2327074;
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MEDLINE=90357780; PubMed=2389555;
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EMBL; U03977; AAA63591.1; -.
PIR; T30879; T30879.
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939 TXPIIFGDFMKVGAEE 954
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 PRELIMINARY;
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Camacho A., Vinuela E.;
"Protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells.";
Virology 181:251-257(1991).
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Virology 188:938-947(1992).
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MEDLINE=22087485; PubMed=1309282;
MCDGIGUES J.M., Salas M.L., Vinuela E.;
"Genes homologous to ubiquitin-conjugating proteins and eukaryotic transcription factor SII in African swine fever virus.";
Virology 186:40-52(1992).
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Garcia-Beato R., Freije J.M.P., Lopez-Otin C., Blasco R., Vinuela
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MEDUINE=9334671; PubMed=8393914;
MEDUINE=9334671; PubMed=8393914;
Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E "African swine fever virus thymidylate kinase gene: Bequence and transcriptional mapping.";
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MEDLINE=90219204; PubMed=2325202;
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MEDLLINE=90219205; PubMed=2325203;
MEDLLINE=90219205; PubMed=2325203;
Gonzalez A., Calvo V., Almazan F., Almendral J.M., Ramirez J.C.,
De La Vega I., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: Family 360.";
J. Virol. 64:2073-2081(1990).
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MEDLINE=93174976; PubMed=8438592;
Manez R.J., Vinuela E.;
"African swine fever virus encodes a DNA ligase.";
Virology 193:531-536(1993).
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STRAIN=BAJ1V;
MEDLINE=93353606; PubMed=8102411;
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"African swine fever virus encodes a CD2 homolog responsible for the adhesion of eythrocytes to infected cells.";
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MEDLINE=937388; PubMed=8503790;
MUROZ M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
Muroz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
Structure and expression in E. coli of the gene coding for protein pl0 of African swine fever virus.";
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Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
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sequence and transcriptional mapping.";
Gene 136:103-110(1993)
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Alcami A., Angulo A., Vinuela B.;
Mapping and sequence of the gene encoding the African swine fever virion protein of Mr. 11500.";
J. Gen. Virol. 74:2317-2324(1993).
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MEDLINE=93327788; PubMed=8335009;
Simon-Mateo C., Andres G., Vinnela E.;
Simon-Certain processing in African swine fever virus: a novel gene expression strategy for a DNA virus.";
EMBO J. 12:2977-2987(1993).
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MEDLINE=94085774; PubMed=8262374;
Yanez R.J., Rodriguez J.M., Boursnell M.E.G., Rodriguez J.F.,
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Pena L., Yanez R.J., Revilla Y., Vinuela E., Salas M.L.;
"African swine fever virus guanylyltransferase.";
Virology 193:319-328(1993).
                                                                                           Nucleic Acids Res. 21:2423-2427(1993).
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SEQUENCE FROM N.A.
MEDLINE=99047670; PubMed=9830033;
MEDLINE=99047670; PubMed=9830033;
Guenzi E., Galli G., Grgurina I., Gross D.C., Grandi G.;
"Characterization of the syringomycin synthetase gene cluster. A link between prokaryotic and eukaryotic peptide synthetases.";
between prokaryotic and eukaryotic peptide synthetases.";
J. Biol., Chem. 273:32857-32863(1998).
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MEDLINE=21820291; PubMed=11831707;
Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
Rodriguez J.F., Vinuela E.,
"Analysis of the complete nucleotide sequence of African swine fever
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GO; GO:0048037; F:cofactor binding; IEA.
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                       "Multigene families in African swine fever virus: family 505."; J. virol. 68:2746-2751(1994).
MEDLINE=94187118; PubMed=8139051;
Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
Vinuela E.;
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Pred. No. 1.6e+02;
5; Mismatches 6; Indels
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Syringomycin synthetase.
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InterPro; IPR008013; AMP-bind.
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InterPro; IPR001142; Condensatu.
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InterPro; IPR00161; Pp bind.
InterPro; IPR01031; Thioesterase.
FEam; PF00501; AMP-binding; 8.
Pfam; PF00668; Condensation; 9.
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MEDLINE=94233765; PubMed=8178480;
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HSSP; P14687; LAMU.
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DR Pfam; PF00550; PF-binding; 9.

DR Pfam; PF00975; Thicosterase; 1.

DR PRINTS; PR00154; Ambalbuning.

DR TIGREAMS; TICR01733; AA-denyl-dom; 8.

DR PROSITE; PS000455; AMP_BINDING; 8.

DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.

DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.

KW Phosphopantetheine.

SQ SEQUENCE 9376 AA; 1029843 MW; P770C08975EP9CE5 CRC64;

Query Match

37.1%; Score 49; DB 2; Length 9376;

Best Local Similarity 43.5%; Pred. No. 1.3e+03;

Matches 10; Conservative 5; Mismatches 8; Indels

QY 1 AGTOPLILAOFMRVGCDELLHFL 23

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No.
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Sequence 20200, Application US/09248796A

Sequence 20200, Application US/09248796A

Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196-1132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1

18-09-128-352-6394

18-09-128-352-6394

Patent No. 6562958

Patent No. 656298

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                          Sequence 224, Appli
Sequence 4, Appli
Sequence 3181, Ap
Sequence 42409, A
Sequence 42409, A
Sequence 4543, Ap
Sequence 15081, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Pred. No. 3.1;
5; Mismatches 12; Indels 1.
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US-09-522-714-18

US-09-710-224

US-09-688-019-4

US-09-602-78-7-588

US-09-134-001C-3171

US-09-328-35-4543

US-09-252-991A-32765

US-09-252-991A-32765

US-09-252-991A-32765

US-09-2810-4

US-09-181-485-4

US-09-181-485-4

US-09-181-485-4

US-09-181-485-4

US-09-181-485-4

US-09-181-485-4
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US-09-328-352-6394
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Best Local Similarity 34.9%;
Matches 15; Conservative
       RESULT 2
US-09-248-796A-20200
          LENGTH
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Length 221;

4, DB

Score 48.5;

30.7%;

TYPE: PRT ORGANISM: Candida albicans

US-09-248-796A-20200

Query Match

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Sequence 17390, Application US/09248796A

Sequence 1730, Application US/09248796A

Patent No. 674137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1939-02-13
PRIOR FILING DATE: 1938-02-13
PRIOR FILING DATE: 1938-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17390
LENGTH: 692
                                                                                                                                                 Sequence 2848, Application US/09540236
Sequence 2848, Application US/09540236
Parent No. 6673910
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: WCLEIC ACLD AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION WUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
WUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
SEQ ID NOS: 3840
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APPLICANT: GARY D. Breton et al.
APPLICANT: GARY D. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 24;
6; Mismatches 9; Indels
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Pred. No. 70;
1; Mismatches 11; Indels
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; Sequence 6395, Application US/09328352
; Patent No. 6562958
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171 NYKAAGDALGIDLLHNP 187
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29.7%;
Best Local Similarity 42.3%;
Matches 11; Conservative 6
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Best Local Similarity 47.8%;
Matches 11; Conservative 1
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; ORGANISM: Candida albicans
US-09-248-796A-17390
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; ORGANISM: M.catarrhalis
US-09-540-236-2848
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                                                                                                        RESULT 5
US-09-540-236-2848
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                                                                                                                                                                                                                                                                                                              ; Sequence 23329, Application US/09252991A; Sequence 23329, Application US/09252991A; Sequence 23329, Application US/09252991A; Sequence 23329, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:

PAPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: US/09/25, 991A; CURRENT APPLICATION NUMBER: US/09/25, 991A; CURRENT FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR PLICATION NUMBER: US/0/094,190; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 23329
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                                         Gaps
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26;
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                                         Indels
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                                     12;
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                                                                                                            2 DTIKGFDLITNFQVV---ADALNISLLPNPLA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
30.4%; Score 48; DB
Best Local Similarity 40.6%; Pred. No. 26;
Matches 13; Conservative 7; Mismatches
   Best Local Similarity 37.5%; Pred. No. 9;
Matches 12; Conservative 5; Mismatches
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Patent No. 6495348
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23329
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Matches 9; Conserv
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Sequence 18090, Application US/09248796A
Sequence 18090, Application US/09248796A
Sequence 18090, Application US/09248796A
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER: 107196.13
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PADELICATION NUMBER: US 60/074,725
PRIOR PADELICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18090
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Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34186, Application US/09270767
; Sequence 34186, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT PAPLICALION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.1e+02;
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Candida albicans
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US-09-270-767-49403
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US-09-270-767-34186
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LENGTH: 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14297, Application US/09489039A
Sequence 14297, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et, al
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TILLE OF INVENTION: PREDMONTAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR PLILOR DATE: 1999-01-29
RIOR APPLICATION NUMBER: US 60/117,747
PRIOR PLILNG DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14297
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3849, Application US/09134000C

| Patent No. 6617156 |
| Patent No. 6617156 |
| GREERAL INFORMATION: |
| APPLICANT: Lynn boucette-Stamm et al |
| TITLE OF INVENTION: WUCEEC ACID AND AMINO ACID SEQUENCES RELATING TO |
| TITLE OF INVENTION: WUCEEC ACID AND AMINO ACID SEQUENCES RELATING TO |
| TITLE OF INVENTION: BUSECCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS |
| CURRENT APPLICATION NUMBER: US/09/134,000C |
| PRIOR APPLICATION NUMBER: US 60/055,778 |
| PRIOR PILING DATE: 1997-08-15 |
| RIOR FILING DATE: 1997-08-15 |
| SEQ ID NOS: 6812 |
| SEQ ID NO 3849 |
| LINGER DE LENGTH 451 |
| WORLD DATE: 1910 |
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Pred. No. 58;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 4; Length 63; Pred. No. 4.4;
                                                                                                                                                                                        Score 46.5; DB 4; Length 5
Pred. No. 58;
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                               1 MDTIKGFDLITNFQV------VADALNISLLPNPLATA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                   ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Enterococcus faecalis US-09-134-000C-3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.1%;
56.5%;
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Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ||| :||| ||
114 LNNFOKIADALTIS 127
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Best Local Similarity 64.3
Matches 9; Conservative
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Matches 13, Conserv
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US-09-489-039A-14297
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US-09-134-000C-3849
SEQ ID NO 6395
LENGTH: 523
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Fri Nov 12 14:55:55 2004

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Sequence 15218, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
FAPELICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.1132
CURRENT APPLICATION NUMBER: US/09/248,796A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
28.5%; Score 45; DB 4; Length 453;
Best Local Similarity 33.3%; Pred. No. 84;
Matches 10; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                            Sequence 3, Application US/09374909;
Patent No. 6603501
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, W. French
Baltrucki, Leon F.
MASON, James M.
TITLE OF INVENTION: Targetable Vector Particles
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,909
FILING DATE: 13-Aug-1999
CLASSIFICATION: UNKNOWN>
APPLICATION NUMBER: 08/484,126
FILING DATE: cUnknown>
APPLICATION NUMBER: 08/484,126
FILING DATE: cUnknown>
APPLICATION NUMBER: 08/973,307
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lillie, Raymond J.
REGISTRATION NUMBER: 31,778
REGISTRATION NUMBER: 31,778
REFERENCE/BOCKET NUMBER: 271010-281
TELECOMMUNICATION INFORMATION:
225 GADPVTRFSLTRQVLNVGPRVPIGPNPVIT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 GADPVTRFSLTRQVLNVGPRVPIGPNPVIT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: xenotropic gp70 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-248-796A-15218
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Pred. No. 84;
5; Mismatches 11; Indels
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Gaps 4.

6 GFDLITNFOVVADALNIS----LLPNPLAT 31

Query Match Best Local Similarity 33.3 Matches 10; Conservative

US-08-484-126-3

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November 11, 2004, 02:43:24; Search time 77.3238 Seconds (without alignments) 146.426 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                               US-10-092-750-67
158
1 MDTIKGFDLITNFQVVADALNISLLPNFLATA 32
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         1568699 segs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodatta/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodatta/2/pubpaa/PCT_MBW_PUB_pep:*
4: /cgn2_6/ptodatta/2/pubpaa/US06_NBW_PUB_pep:*
5: /cgn2_6/ptodatta/2/pubpaa/US06_NBW_PUB_pep:*
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18: /cgn2_6/ptodatta/2/pubpaa/US10D_PUBCOMB_pep:*
19: /cgn2_6/ptodatta/2/pubpaa/US10D_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

đ	67, Appl	156639,	367776,	189678,	122995,	243733,	45323, A	316100,	189437,	42726, A	262020,		242, App
Description	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
QI	US-10-092-750-67	US-10-424-599-156639	US-10-425-115-367776	US-10-424-599-189678	US-10-437-963-122995	US-10-425-115-243733	US-10-425-114-45323	US-10-425-115-316100	US-10-437-963-189437	US-10-767-701-42726	US-10-425-115-262020	US-10-263-929-133.	US-10-267-502-242
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% Query Match Length DB	32	254	171	1097	121	426	435	87	552	207	260	1800	1800
% Query Match	100.0	32.6	32.3	32.3	31.6	31.6	31.6	31.0	31.0	30.7	30.7	30.7	30.7
Score	158	51.5	51	51	50	20	50	49	49	48.5	48.5	48.5	48.5
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10 - 425 - 115 - 3 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 424 - 599 - 1 110 - 425 - 963 - 1 110 - 225 - 625 - 1 110 - 267 - 286 - 1 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 437 - 963 - 1 110 - 425 - 115 - 2 110 - 427 - 599 - 1 110 - 427 - 599 - 1	10-334-143-42 10-437-963-11 10-437-963-12
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## ALIGNMENTS

10-092-750-67

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Gaps
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Sequence 67, Application US/10092750

Sequence 67, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

TITLE OF INVENTOR: POLYPEPTIGES

FILE REFRENCE: 50036/05002

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR PILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 67
LENGTH: 32
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RESULT 2
US-10-424-599-156639
; Sequence 156639, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

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DEPLICANT: LA KOVALICAN:
APPLICANT: LA KOVALICA, Thomas J.
APPLICANT: LA KOVALICA, Thius
APPLICANT: Cao, Vinua
APPLICANT: Cao, Vinua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bribazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Bripazuk, Brad
APPLICANT: Wi, Pin
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122995
LENGTH: 121
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Walcleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION WUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: PAT_MRT3847_142295C.1.pep
US-10-424-599-189678
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US-10-437-963-122995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
32.3%; Score 51; DB 15;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 16;
Pred. No. 14;
                                                                                                                                                                                                                                                     LOCATION: (1)..(1097)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 122995, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 OVVADALNISLLPNPLA 30
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Best Local Similarity 64.7%;
Matches 11; Conservative
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 189678
LENGTH: 1097
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                                                                                                           TYPE: PRT ORGANISM: Glycine max FEATURE: NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-122995
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US-10-425-115-243733
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESQ ID NO 156639
LENGTH: 254
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US-10-424-599-189678
US-10-424-599-189678, Application US/10424599
; Publication No. US20040031072A1
; GENBRAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPRENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT PILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 367776, Application US/10425115
Fublication No. US20040214272A1
Fublication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yondua
APPLICANT: Cao, Yondua
APPLICANT: Cao, Yondua
APPLICANT: Cao, Yondua
APPLICANT: APPLICANT: David K.
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
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APPLICANT: Cao, Yongu
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US-10-424-599-156639
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US-10-425-115-367776
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Sequence 189437, Application US/10437963
; Sequence 189437, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; UNMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)3
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42726
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                   Query Match
31.0%; Score 49; DB 17; Length 87;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 16; Length 55.
Pred. No. 1.3e+02;
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US-10-767-701-42726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_85948C.1.pep
US-10-437-963-189437
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31.0%; Score 49; DB
Best Local Similarity 42.9%; Pred. No. 1.3e
Matches 9; Conservative 5; Mismatches
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30.7%; Score 48.5; D
Best Local Similarity 40.0%; Pred. No. 45;
Matches 12; Conservative 3; Mismatches
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; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic_ David K.
                                                                                                                  11 TNFQVVADALNISLLPNPLATA 32
                                                                                                                                                1 MDTIKGFDLITNFQVVADALN 21
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ORGANISM: Sorghum bicolor
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ORGANISM: Oryza sativa
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; Sequence 316100, Application US/10425115
; Publication Wo. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE REFERENCE: 38-21 (53222)
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316100
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45323, Application US/10425114

| Sequence 45323, Application No. US20040034888A1
| Publication No. US20040034888A1
| Publication No. US2004003488BA1
| GENERAL INFORMATION:
| APPLICANT: Zhou, Yinda
| APPLICANT: Screen, Steven B
| APPLICANT: Go, Yongwei |
| TAPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| CURRENT APPLICATION NUMBER: US/10/425,114 |
| CURRENT PLING DATE: 2003-04-28 |
| SEQ ID NOS: 73128 |
| SEQ ID NOS: 73128 |
| SEQ ID NOS: 73123
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64;
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                                                                                                                                                                                                                                  6; Indels
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US-10-425-114-45323
                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_153867C.1.pep
MS-10-422-115-243733
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                                                                                                                                                                                   Query Match
31.6%; Score 50; DB
Best Local Similarity 43.5%; Pred. No. 64;
Matches 10; Conservative 7; Mismatches
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Best Local Similarity
Matches 10; Conserv
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                            TYPE: PRT
ORGANISM: Zea mays
SEQ ID NO 243733
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-242
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ORGANISM: Zea mays
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US-10-437-963-172368
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APPLICANT:
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                                                                                                                                                    Squares 20200, Application US/10425115

| Saquence 202020, Application US/10425115
| Publication No. US20040214272Al
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Royalic, David K.
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: AUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
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; Sequence 133, Application US/10263929
; Publication No. US20040067535A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; CURRENT APPLICATION NUMBER: US/10/263,929
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 133
; LENGTH: 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.7%; Score 48.5; DB 17;
Best Local Similarity 35.5%; Pred. No. 59;
Matches 11; Conservative 7; Mismatches 10;
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US-10-425-115-262020
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OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
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TVKGFDL------NLVPAPAATA 172
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; ORGANISM: Homo sapiens
US-10-263-929-133
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ORGANISM: Zea mays
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US-10-425-115-262020
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US-10-267-502-242 ; Sequence 242, Application US/10267502 ; Publication No. US20040071700Al ; GENERAL INFORMATION:

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US-10-425-115-355295

US-10-425-115-355295, Application US/10425115

Bublication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Thomas J.

APPLICANT: APOUNT Yihua

APPLICANT: APOUNT Notes Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Notes Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Notes Acid Molecules Associated With

TITLE OF INVENTION: Notes Acid Molecules Associated With

TITLE OF INVENTION: 10-15 (53222)

FILE REPRENCE: 30-15 (53222)

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 355295

LENGTH: 56
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                                                                                    Query Match 30.7%; Score 48.5; DB 15; Best Local Similarity 34.5%; Pred. No. 6.5e+02; Matches 10; Conservative 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87197C.1.pep
US-10-425-115-355295
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Pred. No. 11;
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APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TILE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2
LENGTH: 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DIIKGFDLIINFQVVADALNISLLPNPLA 30
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Sequence 172368, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 52.97
These 9; Conservative
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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172368
; LENGTH: 231
; TYPE: PRT
; CRANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; OCATION: (1)..(231)
; OTHER INFORMATION: Unsure at all Xaa locations
; FEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT4530_70510C.1.pep
US-10-437-963-172368

Query Match
Best Local Similarity 48.3%; Score 48, DB 16; Length 231;
Best Local Similarity 48.3%; Pred. No. 61;
Matches 14; Conservative 2; Mismatches 11; Indels 2; Gaps

OY
6 GFDLITNFQVVADALNISLLDN.-PLATA 32
Db
15 GFDLITNFQVVADALNISLLDN.-PLATA 33
Search completed: November 11, 2004, 07:41:45
Job time: 77.3238 secs
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November 10, 2004, 14:52:32; Search time 10.9324 Seconds (without alignments) 281.634 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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158
1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               283416 seqs, 96216763 residues
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                    Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     Title:
Perfect score: 1
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	hypothetical prote	hypothetical prote	ORF MSV261 leucine	metalloproteinase	myb-related protei	glyceraldehyde-3-p	acetate kinase hom	arginine deiminase	env polyprotein -	collagen alpha 1(I	hypothetical prote	phosphotransferase	hypothetical prote	partial probable s	yegE protein - Esc	hypothetical prote	transcription fact	nasD protein homol	cal	വ	metalloproteinase		NADH dehydrogenase	œ	chitinase B homolo	gen alpha	ager	lagen alpha	
SUMMARIES		C72702	T12739	T28423	A33712	S04899	A49700	AH1220	S02138	VCVWFS	S13580	S55123	AC1204	D90988	F85833	B64973	AH1979	T48518	B64063	T32906	T35345	ZN0892	AH2366	D81219	AB1088	AB1452	B34493	S40495	842617	154
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B47615 AC2644	C97426 B29350	G97253 VCMVSR	G90431	T31203	T07113	VCVWM2	VCVWM1	T22759	AH0297	D69502	S26840	E81450
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29.1	29.1 29.1	29.1 29.1	29.1	29.1	29.1	29.1	29.1	29.1	28.8	28.8	28.8	28.5
44 94 9	4 4 6 6	46 46	46	46	46	46	46	46	45.5	45.5	45.5	45

## ALIGNMENTS

RESULT 1 C72702 hypothetical protein APE1034 - Aeropyrum pernix (strain K1) C72702 C72702 hypothetical protein APE1034 - Aeropyrum pernix (strain K1) C5pecies: Aeropyrum pernix C5pecies: Aeropyrum pernix C5pecies: Aeropyrum pernix C5pecies: C72702 K5, Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 199 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Asreference number: A72450; MUID:9910339; PMID:10382966 A;Accession: C72702 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-321 < KAW> A;Cross-references: UNIPROT:Q9YD78; DDBJ:AP000060; NID:g5104188; PIDN:BAA80019.1; PID:g A;Experimental source: strain K1 C;Genetics: A;Genetics: A;Genetic	; Taka , J.; Aeropy PID:g
Query Match       32.9%;       Score 52;       DB 2;       Length 321;         Best Local Similarity       34.5%;       Pred. No. 6.8;         Matches 10;       Conservative       9;       Mismatches       10;       Indels       0;         Cy       4       IKGFDLITHROVVADALNISLENPLATA       32         Db       270       VEGFDVVPVDEPVVECLQLRLLGHPVARA       298	
RESULT 2  T12739  Hypothetical protein 23 - Methanobacterium phage psiM2 C;Species: Methanobacterium phage psiM2 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T12739 R;Pfister, P:, Wasserfallen, A.; Stettler, R.; Leisinger, T. submitted to the EMBL Data Library, May 1998 A;Description: Archaeophage PsiM2 complete genomic DNA. A;Reference number: Z17578	
d from GB/EMBL APT. UNIPROT:08021 ce: host Metha anobacterium p	DN:AAC
Best Local Similarity 40.5%; Fred. No. 9.2; Matches 13; Conservative 8; Mismatches 8; Indels 3; Gaps 2;	

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Accession: A4970; Barbase, A.; Miretsix, A.; Miretsix, A.; Miretsix, A.; Miretsix, A.; Miretsix, A.; Mueller, M.
J. Mol. Evol. 37, 631-643, 1993
J. Mol. Evol. 37, 631-643, 1993
Aprilles. A glyceraldehyde-3-phosphate dehydrogenase with eubacterial features in the am. A; Reference number: A49700; MUD:94157936; PMID:8114116
A; Molecule type: mRNA
A; Residues: 1-360 < MAR>
A; Accession: B44516
A; A; Accession: B44516
A; Molecule type: mRNA
A; Residues: 11-360 < MUW>
A; Residues: 11-360 < MUW>
A; Residues: 11-360 < MUW>
A; Residues: 11-360 < MUW>
A; Residues: 11-360 < MUW>
A; Cross-references: GB:L11304
B; Muller, M.
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                                                                                                                                                                                                                                                                                    myb-related protein Zm38 - maize

(Species: Zea mays (maize)

(Species: Zea mays (maize)

(Species: Zea mays (maize)

(Space) 1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

(Spacession: 304899

R;Marocco, A.; Wissenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, F.; Rohc

R;Marocco, A.; Wissenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, F.; Rohc

A;Marocco, A.; Wilsenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, F.; Rohc

A;Title: Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the I

A;Reference number: 304899

A;Accession: 504899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Status: 1-255 «MAR»
A;Residues: 1-255 «MAR»
A;Cross-references: UNIPROT:P20025
C;Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology
C;Reywords: DNA binding; duplication; nucleus; transcription regulation
E;9-6112/Domain: myb DNA-binding repeat homology «MYB1»
F;62-112/Domain: myb DNA-binding repeat homology «MYB2»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
30.7%; Score 48.5; DB 1; Length 255;
Best Local Similarity 35.5%; Pred. No. 17;
Matches 11; Conservative 7; Mismatches 10; Indels
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C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD;
F;3-35;Region: beta-alpha-beta NAD nucleotide-binding fold
F;171,198/Active site: Cys, His #status predicted
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399 TVSAYDWITDFQTGIDKIDLSAFRN 423
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A;Molecule type: protein
A;Residues: 1-19,'X',21-63 <MUL>
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Nylternate names: neutral protesse large subunit
(C, Species: Erwinia chrysanthemi
C, Species: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C, Accession: A3312, T48669
R, Pelepelaire, P.; Wandersman, C.
J. Biol. Chem. 264, 9083-9089, 1089
A, Title: Protease secretion by Erwinia chrysanthemi. Proteases B and C are synthesized A, Accession: A3312; MUD:89255387; PMID:2722818
A, Reference number: A33712; MUD:89255387; PMID:2722818
A, Residues: DELA
A, Residues: 1-411 c.DELA
A, Residues: 1-411 c.DELA
A, Residues: 1-411 c.DELA
A, Residues: 1-411 c.DELA
A, Residues: 1-421 c.DELA
A, Residues: 1-431 c.DELA
A, Residues: 1-4
                                                                                                                                                                                                                                                                                           RESULT 3
T28423
ORF MSV261 leucine rich repeat gene family protein - Melanoplus sanguinipes entomopoxvir
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Melanoplus sanguinipes entomopovirus
C;Species: Melanoplus sanguinipes entomopovirus
C;Date: 21-dan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28423
N;Afitie: The genome of Melanoplus sanguinipes entomopovirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28423
A;Accession: T2843

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Pred. No. 31;
6; Mismatches 10; Indels
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      DTIKGFDLITNF--QVVADALNISLLPNPLAT 31
                                                                           29 DTIKGYAILKNTGDEVIEDLL-IMPVPDFFAS 59
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Pred. No. 25;
4; Mismatches
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Best Local Similarity 38.7%;
Matches 12; Conservative
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Best Local Similarity 36.0%;
Matches 9; Conservative 6
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NyAlternate names: procollagen alpha 1(IX) chain, long splice form
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S13580; S2195; S2140; C35980; S21087; S74294
Eur. J. Biochem. 192, 703-708, 1990
A;Title: The complete primary structure of two distinct forms of human alpha-1(IX) coll
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Residues: 1-931 kMTA
A;Title: The molecular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pr
A;Title: The molecular biology of collagens with short triple-helical domains.
A;Reference number: S2243
A;Reference number: S2243
A;Reference muber: S22243
A;Reference muber: S22243
A;Reference muber: S22245
A;Residues: 1-253, VV, 255-815;835-884 kNIN>
A;Residues: 1-253, VV, 255-815;835-884 kNIN>
A;Residues: 1-253, VV, 255-815;835-884 kNIN>
B;Kimira, T.; Mattei, M.G.; Stevens, J.W.; Goldring, M.B.; Ninomiya, Y.; Olsen, B.R.
Eur. J. Blochem. 179, 71-70, 1989
A;Title: Molecular cloning of rat and human type IX collagen cDNA and localization of the approach of the contract number: S02140; MUID:89137096; PMID:2465149
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 580-596;598-620, KR, 622-813;835-884 «KIM>
B;Muragaki, Y.; Nishimura, I.; Henney, A.; Ninomiya, Y.; Olsen, Proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990
A;ittle: The alphal(IX) collagen gene gives rise to two different A;Reference number: A35980; MUID:90207204; PMID:1690886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 36.7%; Pred. No. 60;
Local Similarity 36.7%; Pred. No. 60;
Les 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 GIDPVTRFSLTRQVLNIGPRLPIGPNPVIT 241
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species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dlate: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02138; B8299
R;Baur, H; Lucchi, E.; Stalon, V; Mercenier, A.; Haas, D.
Eur, J; Bicchem: 179; 53-60, 1989
A;Title: Sequence analysis and expression of the arginine-deiminase and carbamate-kinase
A;Reference number: S02137; MUD:89137094; PMID:2537202
A;Reference number: S02137; MUD:89137094; PMID:2537202
A;Residues: 1-418 <a href="https://docs.org/references-number: barbar-his-lange-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repart-organis-repar
acetate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Datcession: AH1220
C;Accession: AH1220
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, D.; Jones, L.M.; Karsft, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simcos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: L.397 <GLA>
A;Cross-references: UNIPROT:QSY7V1; GB:NC_003210; PIDN:CAC99246.1; PID:g16410584; GSPDB:
A;Cross-references: UNIPROT:GST7V1; GB:NC_003210; PIDN:CAC99246.1; PID:g16410584; GSPDB:
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Csbyerfamily: arginine deiminase arcA
C;Keywords: hydrolase
F;2-418/Product: arginine deiminase #status predicted <MAT>
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C;Superfamily: Acetate/propionate kinase
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C,Accession: AC1204
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Doninquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; McAuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; McAuthors: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A; Accession: D9088
A; Molecule type: DNA
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A; Residue: 1-791 cHAX>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:Q8Y882; GB:NC_003210; PIDN:CAC99113.1; PID:g16410437; GSPDB
A,Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                   phosphotransferase system (PTS) beta-glucoside-specific enzyme IIABC homolog lmo1035
                                                                                                                                                                                                                                                                                                                                             C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific;
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C;Superfamily: Signal transduction protein with an integral membrane
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                                                  1 MDTIK--GFD-----LITNFQVVADALNISL 24
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Best Local Similarity 48.3%; Pred. No. 92;
Matches 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47.5;
Pred. No. 69;
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1 MDTIKG--FDLITNFQVVADALNISLLPNP
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Best Local Similarity 35.5:
Matches 11; Conservative
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A;Molecule type: DNA
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hypothetical protein YMR176w - yeast (Saccharomyces cerevisiae)

hypothetical protein YMR010.06

c)Species: Saccharomyces cerevisiae

C)Dates: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C)Accession: S55123

R/Churcher, C.M.

submitted to the EMBL Data Library, June 1995

A;Reference number: S5518

A;Accession: S5513

A;Molecule type: DNA

A;Reference number: S5118

A;Cross-references: UNIPROT: Q03214; EMBL: Z49808; NID: 9854440; PIDN: CAA89909.1; PID: 98544

A;Experimental source: strain AB972

C;Genetics:
C;Genetics:
A;Cross-references: SGD: SGD: S0004788; MIPS: YMR176w

A;Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Function: structural component of extracellular fibrous polymer associated with type Mode: in chondrocytes the long splice form is predominantly produced for Mode: in chondrocytes the long splice form is predominantly produced for Mode: alternative splicing; coiled coil; extracellular matrix; glycoprotein; heter in 23/Domain: signal sequence #status predicted <SIG.*
19.4-28/Domain: signal sequence #status predicted <NIC4*
19.4-28/Domain: non-collagenous NO3 #status predicted <OL3*
19.6-405/Domain: non-collagenous CO13 #status predicted <COL3*
19.6-417/Domain: collagenous CO12 #status predicted <NC3*
19.7-57/Domain: collagenous CO12 #status predicted <NC3*
19.7-901/Domain: collagenous CO12 #status predicted <NC3*
19.7-901/Domain: non-collagenous NO1 #status predicted <NC3*
19.7-901/Domain: non-collagenous NO1 #status predicted <NC1*
19.2-931/Domain: non-collagenous NO1 #status predicted <NC1*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 6q12-6q14
A,Introns: 5/2; 232/3; 260/3; 267/3
C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(
                                                                                                                                                                                                                                                                                                        , Molecule type: DNA
, Residues: 14,233-248, Tr,250-267 < OLS>
, Cross-references: EMBL:M32135
, Diab, M.; Wu, J.J.; Eyre, D.R.
loohem, U. 314, 327-332, 199 
Title: Collagen type IX from human cartilage: a structural profile of intermolecular
, Reference number: $64673; MUID:96195147; PMID:8660302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: S74294
A, Molecule type: protein
A, Residues: 405-417 ADIA>
C, Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently 0-glycosylated.
C, Genetics:
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Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                      ubmitted to the EMBL Data Library, February 1990; Reference number: $21087; Accession: $21087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Gene: GDB:COL9Al
;Cross-references: GDB:119794; OMIM:120210
                                         Residues: 1-4,233-267 <MUR2>
Cross-references: EMBL:M32135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : ||||| : ||||
DDLPGFDLISQFQV 65
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Matches
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phosphotransferase

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Gaps

7;

Indels

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domain and Pas,

7

Gaps

Indels

C; Accession: F85833 R; Perna, N.T.; Plunk

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A,Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A,Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A,Rotecesion: R65833

A,Status: preliminary

A,Molecule type: DNA

A,Residues: 1-935 < CATO-

A,Cross-references: UNIPROT: Q8X7K1; GB:AB005174; NID:g12516270; PIDN:AAG57130.1; GSPDB:G

A,Experimental source: strain 0157:H7, substrain EDL933

A,Genei: 23236

C,Geneiics:

A,Genei: 23236

C,Superfamily: Signal transduction protein with an integral membrane domain and Pas, GGP
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
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Cjaccession: B64973 C. Riley, C. R. Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co Science P. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co Science 277, 1453-1462, 1997 C. Requence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B64973 ggE protein - Escherichia coli (strain K-12)
Species: Escherichia coli
Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 16-Aug-2004

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: Molecule type: M

1071 MDTLSGIGVDLIYG-EVIADAQPLDLLVN 1098 1 MDTIKGF--DLITNFOVVADALNISLLPN 27 a à

'n

3; Gaps

Score 47.5; DB 2; Length 1105; Pred. No. 1.4e+02; 4; Mismatches 8; Indels 3

Query Match
Best Local Similarity 48.3%;
Matches 14; Conservative

Search completed: November 10, 2004, 15:55:05 Job time: 11.9324 secs

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us-10-092-750-67.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 53.637 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

.US-10-092-750-67 158 1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	1	Q612h0 picrophilus			Q61q81 photobacter	4	Q85506 murine leuk	Q6njy2 corynebacte	Cae48764 corynebac	Q74nj5 nanoarchaeu	Aar39201 nanoarcha	O80213 methanobact		Q8kcf2 chlorobium			Q9yvil melanoplus	Q6nix8 corynebacte	S			Q6btd4 debaryomyce	Q9rhj8 streptomyce	Q71sz2 scombridae	Aag14279 scombrida	O50152 streptomyce	Q896z2 clostridium	P16316 erwinia chr	7 rmx3	6£1£9 1	Q88914 pseudomonas
SOLVENING	ΩΙ	Q6CON9	Ф612Н0	Q9YD78	Q6D3R8	Q6LQ81	CAG20545	085506	Q6NJY2	CAE48764	Q74NJ5	AAR39201	080213	036002	Q8KCF2	QEFCVO	Q6FA70	Q9YVI1	O6N1X8	CAE49155	Q7RH86	Q6FR20	Q6BTD4	ОЭКНЈВ	071822	AAQ14279	050152	Q896Z2	PRTB_ERWCH	Q7RMX3	Q6F1T9	088914
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*	Query Match		33.5	32.9	32.9	•	32	32.9	32.9	32.9	32.3	32.3	32.0	32.0	32.0	32.0	32.0	32.0	н	31.6	$\overline{}$	31,6	$\vdash$	31.0	31.0	31.0	31.0	31.0	•	31.0	31.0	30.7
	Score	57.	53	52	52	52	52 .	52	52	52	51	51	ö	ö	50.5		ö	ö	20	20	20	20	20	49			49	4.9	49	49	49	48.5
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P20025 zea mays (m 01556 trichomonas Q27820 trichomonas Q27820 trichomonas Q77821 listeria mo Q7202 listeria mo Q8471 clostridium Q8471 clostridium Q8471 clostridium Q85248 homo sapien Q7mtp3 porphyromon Q7mtp3 porphyromon Q78149 planomonos Bad08678 planomono Q81d93 plasmodium	
MYB3 MAIZE 015556 027820 072782 072782 072072 0894M1 0954H2 NU98 HUMAN 07MTP3 0750W4 BAD08678	
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255 325 3350 3350 3350 3397 1729 1103 1113	
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4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	

## ALIGNMENTS

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STRAIN-SCRII043;
Bell K. S., Sebalita M., Pritchard L., Holden M., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Praser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D., Valle G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                           01-0CT-2004 (TrEWBLrel. 28, Created)
01-0CT-2004 (TrEWBLrel. 28, Last sequence update)
01-0CT-2004 (TrEWBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putrescine transport 38, Last annotation update)
Name=potG; ORFNames=ECA2676;
Barteria; Proteobacteria; arroseptica SCRI1043.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBirel. 27, Created)
05-JUL-2004 (TrEMBirel. 27, Last sequence update)
05-JUL-2004 (TrEMBirel. 27, Last annotation update)
Putative Na+/H+ antiporter.
Name=MW2219: OrderedLocusNames=PBFRA2147;
Photobaccerium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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Best Local Similarity 45.5%; Pred. No. 76;
Matches 10; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 377;
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378670; CAG20545.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 AA; 41989 MW; 4B24588EC144C50A CRC64;
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270 VEGFDVVPVDEPVVECLQLRLLGHPVARA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro, IPR004770; Antiport_nhaC.
Interpro, IPR011014; MSCS_transmembr.
Pfam, PF0353; Na H_antiporter; 1.
TIGRPAMS; TIGR00931; antiport_nhaC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 IKGFDLITNFQVVADALNISLLP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LAGFELPTQGQIVLDGQDLSLVP 87
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 487 AA;
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Q6LQ81;
                                                                                                              Q6D3R8
Q6D3R8;
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                                                                                                                                                                                                                                                                                                        Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C., Schepers B., Dock C., Antranikian G., Liebl W., "Genome sequence of Picrophilus torridus and its implications for life around pH 0.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE 99310339; PubMed=10382966; MEDLINE 99310339; PubMed=10382966; Kawarabayagai Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayagai Y., Hino Y., Horikawa S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Fundhashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Kubota K., Crenarchaeon, Aeropyrum pernix Kl."; Marayamiic
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32.9%; Score 52; DB 2; Length 321;
Best Local Similarity 34.5%; Pred. No. 49;
Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                            Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales,
Picrophilaceae, Picrophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%; Score 53; DB 2; Length 309; 42.3%; Pred. No. 34; tive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hypothetical protein.
SEOUENCE 321 AA; 35976 MW; P55FB92792299ClD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA; 34736 MW; 79E14F6540759692 CRC64;
                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Muramoyletrapeptide carboxypeptidase (EC 3.4.17.13)
OrderedLocusNames=PT00247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ABE1034.
OrderedLocusNames=APE1034;
                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096 (2004).

EMBL, AE01261; AAT42832.1; --
GO, GO:0004180; P:carboxypeptidase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR003507; Peptidase U61.

Pfam; PF02016; Peptidase_U61; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete protecme; Hydrolase.
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                            (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                              Picrophilus torridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carboxypeptidase;
SEQUENCE 309 AA
                                                                                                                                                                                                             NCBI_TaxID=82076;
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                               -JUL-2004
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STRAIN=K1;
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CAE48764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome Analysis of Photobacterium profundum reveals the complexity of
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"Analysis of the env gene of a molecularly cloned and biologically active Moloney mink cell focus-forming proviral DNA.";

J. Virol. 44:19-31(1982)

EMBL; J02254; AAA46517.1; -.

HSSP; PO3385; LMOF.

GO, GO:0019028; C:viral capsid; IEA.

GO, GO:0010028; F:structural molecule activity; IEA.

InterPro; IPR002050; Env polyprotein.

InterPro; IPR00881; FMLVrecept-bind.
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MEDLINE-83059868; PubMed-7143566;
Bosselman R.A., van Straaten F., van Beveren C.P., Verma I.M.,
                                                                                                                                                                                                                                                                                                                                                                                                               Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 487;
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR379670; CAG20645.1; -.
SEQUENCE 487 AA; 51332 MW; D56453B148B800DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Env polyprotein.
Murine leukemia virus.
Viruses; Retrovid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Potential.
FB242484A547CA81 CRC64;
                                                                                                                                                                                                                                                    10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Purative Na+/H+ antiporter.
MW2219 OR PBPRA2147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095506; Q85508;
01-NOV-1996 (TERBLE). 01, Created)
01-NOV-1996 (TERBLE). 01, Last sequence update)
01-MAR-2004 (TERBLE). 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 32.9%; Score 52; DB 2; Local Similarity 45.5%; Pred. No. 76; les 10; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 AA.
277 VQGFSLQQGFQAYVDGFNISML 298
                                                                                                                                                                                               PRT;
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636 AA; 69461 MW;
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                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE
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MEDLINE=22965443; PubMed=14602910;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DNA polymerase III subunit gamma/tau (EC 2.7.7.7).
Name=dnaX; Synonyms=dnaZX; OrderedLocusNames=DIP0259;
Corynabacterium diphtheriae.
Corynabacteria, Actinobacteridae; Actinomycetales;
Corynabacterineae; Corynabacteriaceae; Corynabacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI TaxID=1717,
         Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 707;
                                                                                               10; Indels
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CAE48764,
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DNAR-2004 (TrEMBLrel. 27, Last annotation update)
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)
DNAX OR DNAXX OR DIPOZS)
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41.9%; Pred. No. 1.1e+02;
ive 3; Mismatches 15;
Score 52; DB 2;
Pred. No. 1e+02;
4; Mismatches 1
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         32.9%;
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    Query Match
Best Local Similarity 40.0
Matches 12; Conservative
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STRAIN=Kin4-M;
MEDLINE=22946215; PubMed=14566062;
Waters E., Hohn M.J., Abel I., Graham D.E., Adams M.D., Barnstead M.,
Baeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
Bathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,
Soell D., Stetter K.O., Short J.M., Noorderwier M.;
"The genome of Nanoarchaeum equitans: insights into early archaeal
evolution and derived parasitism.";
Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).
EMBL; AE017199; AAR39201.1; -.
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STRAIN=NS-1PRR AICC 50210;
MEDLINE=98360012; PubMed=9694668;
Viscogliosi E., Muller N.;
"Phylogenetic relationships of the glycolytic enzyme, glyceraldehyde-3-phosphate dehydrogenase, from parabasalid flagellates.";
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein.
Methanobacterium phage psiM2.
Viruses; dsDM3 viruses, no RNA stage; Caudovirales; Siphoviridae.
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MEDLITHS=98009532, PubMed=9791169;
MEDLITHS=98009532, PubMed=9791169;
Pfister P., Wasserfallen A., Stettler R., Leisinger T.;
Molecular analysis of Methanobacterium phage psiM2.";
Mol. Microbiol. 30:233-244(1998).
EMBL, AF066411; AAC27062.1; ---
PIR; T12739; T12739.
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Eukaryota, Parabasalidea, Trichomonada, Trichomonadida,
Monocercomonadidae, Monocercomonas.
NCBI_TaxID=5737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
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Local Similarity 40.6%; Pred. No. 68;
les 13; Conservative 8; Mismatches
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STRAIN-KIN-H-M;
MEDLINB-2246215; PubMed=14566062;
MEDLINB-2246215; PubMed=14566062;
MELS E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M., Becson K.Y., Bibbs I., Bolanos R., Keller M., Kretz K., Lin X., Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M., Soell D., Stetter K.O., Short J.M., Noorderwier M.;
"The genome of Nanoarchaeum equitans: insights into early archaeal evolution and derived parsatitism."
Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).
EMBL. AEU7199; AAR32201.1;
InterPro., IPR002749; DUF63.
Pfam, PP01889; DUF63; 1.
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NCBI_TaxID=160232;
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Archaea; Nanoarchaeota; Nanoarchaeum.
NCBI_TaxID=160232;
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Matches 12; Conservative
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SEQUENCE 209 AA
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Query Match

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NEQ352

RESULT 11 AAR39201 **NEQ352** 

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Gaps

232 TVKGFNLLTGFPDTQEISTAVLREIITTPL 261

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Job time : 55.7139 secs
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InterPro; P:glycolysis; IEA.

InterPro; IRR000173; GAP dhdrogenase.

Pfam; PF02800; Gp dh C; I.

Pfam; PF02800; Gp dh C; I.

PRINTS; PR00078; G3PBHRGNASE.

PROSITE; PS00071; GAPDH; 1.

ROYCLYS; NAD; Oxidoreductase.

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C STRAIN=TLS / ATCC 49652 / DSM 12025;

X MEDLINE=221036885; PubMed=12093901; DOI=10.1073/pnas.132181499;

A BIDLINE=221036885; PubMed=12093901; DOI=10.1073/pnas.132181499;

A Bisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F., A Hickey E.K., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H.M., White O., Gruber T.M., The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

R FIGR: CT1470;
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J. Mol. Evol. 47:190-199(1998).
-!- CATALTIA GATIVITY: D-GLYCeraldehyde 3-phosphate + phosphate + NAD(+) = 3-phospho-0-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- STBUTIT: Homotetramer (By similarity).
-!- SUBCELLIULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate dehydogenase family.
--- EMBL; AF022420; AAC63603.1; --- HSSP; P17721; LHDG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia, Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              323 AA; 34604 MW; 3F6DBF17FB5C6792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 AA; 37973 MW; 7A7211FF855C625E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rod shape-determining protein MreB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.0%; Score 50.5; D: 41.4%; Pred. No. 83; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.0%; Score 50.5; D
36.7%; Pred. No. 90;
iive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 MDPIVSSDIIDDNHSSIVDGLSTMVLPNP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDTIKGFDLI-TNFQVVADALNISLLPNP 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=mreB-2; OrderedLocusNames=CT1470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; 1PK004753; MreB Mrl. Pfam; PF06723; MreB Mbl; 1. PRINTS; PR01652; SHĀPEPROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlorobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8KCF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q8KCF2
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Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,

Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,

A Labarre L., Cruveller S., Robert C., Durat S., Wincker P.,

Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;

Indique features revealed by the genome sequence of Acinetobacter sp.

Thique features revealed by the genome sequence of Acinetobacter sp.

Thoric Acids Res. 0:0-0(2004).

Nucleic Acids Res. 0:0-0(2004).

Nucleic Acids Res. 0:0-0(2004).

Rembl. (R543861; CAG68109.1; --

DR InterPro; IPR001037; FAD. Dyr.redox.

DR InterPro; IPR00100; Pyr.redox.

DR InterPro; IPR00142; Rng mnoxygenase.
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05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
Alvyl hydroperoxide reductase amontation update)
Name-ahp? OrderedLocusNames-ACIAD1234;
Aduntchbacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 32.0%; Score 50.5; DB 2; Length 5. Local Similarity 32.6%; Pred. No. 1.4e+02; les 14; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 LNQIKGLNLKADFDVFVSLSCHNCPDVVQALNLIAIYNPNSTA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERMI, PP00170; Pyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00369; PADPRT
PRINTS; PR00469; PNDROTASEI.
PRINTS; PR00469; PNDROTASEII.
PRINTS; PR00420; RNGMNOXGNASE.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
COMPIETE PROCESSER:
SEQUENCE 519 AA; 55803 MW; 0CA26DB974FA8F18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDTIKGFDLITNFOV------VADALNISLLPNPLATA 32
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Sequence 3, Appli
Sequence 9204, Ap
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Sequence 5257, Ap
Sequence 12278, A
Sequence 1080, Ap
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Sequence 3778, Ap
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Sequence 3788, Ap
Sequence 3778, Ap
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                                                                                                                                                                                                                                                                         Sequence 246, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
  09-148-545-246
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GENERAL INFORMATION: 70 Human Secreted Proteins TITLE OF INVENTION: 70 Human Secreted Proteins TITLE OF INVENTION: 70 Human Secreted Proteins TITLE OF INVENTION: 70 Human Secreted Proteins CURRENT APPLICATION NUMBER: US/09/148,545 CURRENT FILING DATE: 1998-09-04

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ERRLIER FILING DATE: 1997-03-07

ERRLIER PILING DATE: 1997-05-23

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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABPLICANT: LYND DOUGETE-Stamm et al ADRIGO ACID SEQUENCES RELATING TO TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCOCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFRENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/0134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-06-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.9%; Score 49.5; DB 4; Length 352; 40.0%; Pred. No. 3.9; ive 4; Mismatches 6; Indels
                                                                                                                                                                        Length 339;
                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                                                                                          Mismatches
                                                                                                                                                                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 TWGLLGSMPTMEGTEDKLYAIPGSP 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TW-----MKTLQGLLDRIQAFPSSP 21
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5243, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Enterococcus faecalis
US-09-134-000C-5243
                                                                                                                                                                                                                                                                                                                223 TWQQALTGLLERMOTY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative 4
                                                                                                                                                                                                                                                                  2 TWMKTLQGLLDRIQAF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 40.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-000C-5243
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LENGTH: 352
                                                                                              SEQ ID NO 246
LENGTH: 339
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.8%; Score 47; DB 4; Length 369; 42.9%; Pred. No. 11; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGRYT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-8077
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 5270:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (B) L\overline{\rm O}CATION 1...369 SEQUENCE DESCRIPTION: SEQ ID NO: 5270:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINES SOURCES (Recium
ORGANISM: Enterococcus faecium
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: LYNN A DOUCETTE-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 TWRVTVQGISDRKTVFNPTNH 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TWMKTLQGLLDRIQAFPSSPH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: July 2, 1 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR SEQ ID NO: 7093:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (781)893-50
TELEFAX: (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
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Matches 9; Conservative
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Sequence 5, Application US/09407427
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LENGTH: 732
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APPLICANT: Acton, Susan L.
APPLICANT: Acton, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
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COUNTRY: USA

CONPUTER: D02109-100

COMPUTER: DEN PC compatible
COMPUTER: DEN PC compatible
COMPUTER: DEN PC compatible
COMPUTER: DEN PC compatible
CORREATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION NUMBER: B14
ATTORNEY/AGNET INFORMATION:
NAME: Arnold E., Beth
REGISTRATION NUMBER: 35-430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELEFONE: 617-832-1000
TELEFONE: 617-832-1000
TELEFAX: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                 Query Match
39.4%; Score 46.5; D
Best Local Similarity 44.0%; Pred. No. 13;
Matches 11; Conservative 1; Mismatches
                                                                                                                                                      ), NAME/KEY: misc feature LOCATION: (B) LOCATION 1...362; SEQUENCE DESCRIPTION: SEQ ID NO: 7093: US-09-107-532A-7093
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGHAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 TWGLLGSMPTLDSANDRLYAIPGSP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TW-----MKTLQGLLDRIQAFPSSP 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08989299
Patent No. 6194556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 WMKTLQGLLDRIQAFPSSPH 22
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US-08-989-299-5
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RESULT 6 US-09-407-427-5

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APPLICANT ACCOUNTS.

AND INCORPTION.

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AND INCORPTION.

AND INCORPTION.

AND INCORPRION.

AND IN
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APPLICANT: Acton, Sugan L.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
FILE REPERENCE: MNI-132CP.
CURRENT PAPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 08/163,648
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-0-30
PRIOR FILING DATE: 1999-12-11
                             Sequence 9, Application US/08989299
Patent No. 6194556
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: RObinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR INUMBER OF SEQUENCES: IN THE APPLICANT AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR ORRESPORDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
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                                                                                                                                                                                                                                                                                      CITY:
STATE: MA
COUNTRY: USA
ZIP: 0.109-2170
ZIP: 0.109-2170
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: Parcentin Release #1.0, Version #1.30
SOFTWARE: Parcentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ARTON NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-7000
TELEPHONE: 617-832-7000
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09407427
Patent No. 6610497
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36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-299-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES.

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27554
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APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
AITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR PELING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
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  Length 1312;
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38.1%; Score 45; DB 4; Length 349;
Best Local Similarity 47.1%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                 8; Indels
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  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.0%; Score 46; DB Best Local Similarity 35.0%; Pred. No. 69; Matches 7; Conservative 5; Mismatches
Query Match 39.0%; Score 46; DB Best Local Similarity 35.0%; Pred. No. 69; Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27544, Application US/09252991A Patent No. 6551795
                                                                                                                           889 WAQTWSNIYDLVAPFPSAPN 908
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                                                                                             3 WMKTLQGLLDRIQAFPSSPH 22
                                                                                                                                                                                                                                                      Sequence 8, Application US/09407427
Patent No. 6610497
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261 ATWSQALQAAIRQIQAY 277
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CORGANISM: Murine sp.
US-09-407-427-8
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CRGANISM: Pseudor
US-09-252-991A-27544
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
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US-09-621-976-4517
                                                                                                  US-09-538-092-1136
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US-09-538-092-1136

Sequence 1136, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Gloct, Loic

APPLICANT: Mansfield, Traci A.

TILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR PRING DATE: 1999-04-01

PRIOR PRING DATE: 2000-02-01

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR PRING DATE: 1399-04-01

SOFTWARE OF SEQ ID NOS: 1136

SOFTWARE CURABATES CURABATES CURRENT OF 1387

SOFTWARE: CURABATES CURABATES CURBER: 2000-02-01

HOWER OF 1136

SOFTWARE: CURABATES CURBATES CONTACT OF SEQ ID NO 1136

HOWER OF 1136
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; LOCATION: (239)

; OCHER INFORMATION: Description of Artificial Sequence: Full length

; OTHER INFORMATION: utrophin construct; Xaa = unknown

US-09-091-501B-10
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                                             Query Match 38.1%; Score 45; DB 4; Length 1313; Best Local Similarity 36.8%; Pred. No. 1e+02; Matches 7; Conservative 4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCHEMENTION:
APPLICANT: Tinaley, Jonathon M
APPLICANT: Tinaley, Jonathon M
APPLICANT: Davies, Kay E
ITLE OF INVENTION: Utrophin gene expression
FILE REPERBORCE: 620-42
CURRENT APPLICATION NUMBER: US/09/091,501B
CURRENT FILING DATE: 1998-06-18
FRIOR APPLICATION NUMBER: PCT/GB96/03156
FRIOR APPLICATION NUMBER: GB 9525962.8
FRIOR FILING DATE: 1996-12-19
FRIOR FILING DATE: 1996-12-19
FRIOR FILING DATE: 1996-07-26
FRIOR FILING DATE: 1996-07-26
FRIOR APPLICATION NUMBER: GB 9615797.9
FRIOR FILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTHARE: PALENTI VET. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                      RESULT 12
US-09-031-501B-10
US-09-031-501B-10
; Sequence 10, Application US/09091501B
; Patent No. 6518413
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-407-427-9
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                                                                                                                                                                       Length 3433;
                                                                                                                                                                    Query Match 38.1%; Score 45; DB 4; Length 343
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4517, Application US/09621976
; Sequence 4517, Application US/09621976
; Patent No. 6639063
; GENERAL INPORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET. 054PR2
; CURRENT APPLICANTON WUMBER: US/09/621,976
; CURRENT APPLICANTON NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; LENGTH: 153
; TYPE: PRT
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P46939
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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins FILE REFERENCE: PZO10P1
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Pred. No. 10;
6; Mismatches
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CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1998-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER PAPPLICATION NUMBER: 60/052,803
EARLIER PAPPLICATION NUMBER: 60/052,803
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APPLICATION NUMBER: 60/051,931
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US-09-277-357-617
Sequence 617, Application US/09227357
Patent No. 6342581
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112 LKTL-GVLEKIQAYPEA 127
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Best Local Similarity 52.9%;
Matches 9; Conservative (
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